

A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM THE
GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA LIBRARY
APPLICATION TO THE DETECTION OF MYCOBACTERIA

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I. Background of the invention

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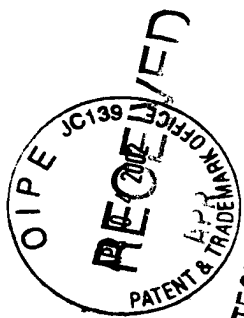
[001] The present invention pertains to a method for isolating a polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and that is absent or altered in the genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone belonging to a genomic DNA library of a given mycobacterium strain, said DNA library being cloned in a bacterial artificial chromosome (BAC). The invention concerns also polynucleotides identified by the above method, as well as detection methods for mycobacteria, particularly *Mycobacterium tuberculosis*, and kits using said polynucleotides as primers or probes. Finally, the invention deals with BAC-based mycobacterium DNA libraries used in the method according to the invention and particularly BAC-based *Mycobacterium tuberculosis* and *Mycobacterium bovis* BCG DNA libraries.

[002] Radical measures are required to prevent the grim predictions of the World Health Organisation for the evolution of the global tuberculosis epidemic in the next century becoming a tragic reality. The powerful combination of genomics and bioinformatics is providing a wealth of information about the etiologic agent, *Mycobacterium tuberculosis*, that will facilitate the conception and development of new therapies. The start point for genome sequencing was the integrated map of the 4.4 Mb circular chromosome of the widely-used, virulent reference strain, *M. tuberculosis* H37Rv and appropriate cosmids were subjected to systematic shotgun sequence analysis at the Sanger Centre.

[003] Cosmid clones (Balasubramanian et al., 1996; Pavelka et al., 1996) have played a crucial role in the *M. tuberculosis* H37Rv genome sequencing project. However, problems such as under-representation of certain regions of the chromosome, unstable inserts and the relatively small insert size complicated the production of a comprehensive set of canonical cosmids representing the entire genome.

II. Summary of the invention

[004] In order to avoid the numerous technical constraints encountered in the state of the art, as described hereabove, when using genomic mycobacterial DNA libraries constructed in cosmid clones, the inventors have attempted to realize genomic



mycobacterial DNA libraries in an alternative type of vectors, namely Bacterial Artificial Chromosome (BAC) vectors.

[005] The success of this approach depended on whether the resulting BAC clones could maintain large mycobacterial DNA inserts. There are various reports describing the successful construction of a BAC library for eucaryotic organisms (Cai et al., 1995; Kim et al., 1996; Misumi et al., 1997; Woo et al., 1994; Zimmer et al., 1997) where inserts up to 725 kb (Zimmer et al., 1997) were cloned and stably maintained in the *E. coli* host strain.

[006] Here, it is shown that, surprisingly, the BAC system can also be used for mycobacterial DNA, as 70% of the clones contained inserts in the size of 25 to 104 kb.

[007] This is the first time that bacterial, and specifically mycobacterial, DNA is cloned in such BAC vectors.

[008] In an attempt to obtain complete coverage of the genome with a minimal overlapping set of clones, a Bacterial Artificial Chromosome (BAC) library of *M. tuberculosis* was constructed, using the vector pBeloBAC11 (Kim et al., 1996) which combines a simple phenotypic screen for recombinant clones with the stable propagation of large inserts (Shizuya et al., 1992). The BAC cloning system is based on the *E. coli* F-factor, whose replication is strictly controlled and thus ensures stable maintenance of large constructs (Willems et al., 1987). BACs have been widely used for cloning of DNA from various eucaryotic species (Cai et al., 1995; Kim et al., 1996; Misumi et al., 1997; Woo et al., 1994; Zimmer et al., 1997). In contrast, to our knowledge this report describes the first attempt to use the BAC system for cloning bacterial DNA.

[009] A central advantage of the BAC cloning system over cosmid vectors used in prior art is that the F-plasmid is present in only one or a maximum of two copies per cell, reducing the potential for recombination between DNA fragments and, more importantly, avoiding the lethal overexpression of cloned bacterial genes. However, the presence of the BAC as just a single copy means that plasmid DNA has to be extracted from a large volume of culture to obtain sufficient DNA for sequencing and it is described here in the examples a simplified protocol to achieve this.

[010] Further, the stability and fidelity of maintenance of the clones in the BAC library represent ideal characteristics for the identification of genomic differences possibly responsible for phenotypic variations in different mycobacterial species.

[011] As it will be shown herein, BACs can be allied with conventional hybridization techniques for refined analyses of genomes and transcriptional activity from different mycobacterial species.

[012] Having established a reliable procedure to screen for genomic polymorphisms, it is now possible to conduct these comparisons on a more systematic basis than in prior art using representative BACs throughout the chromosome and genomic DNA from a variety of mycobacterial species.

[013] As another approach to display genomic polymorphisms, the inventors have also started to use selected H37Rv BACs for "molecular combing" experiments in combination with fluorescent *in situ* hybridization (Bensimon et al., 1994; Michalet et al., 1997). With such techniques the one skilled in the art is enabled to explore the genome of mycobacteria in general and of *M. tuberculosis* in particular for further polymorphic regions.

[014] The availability of BAC-based genomic mycobacterial DNA libraries constructed by the inventors have allowed them to design methods and means both useful to identify genomic regions of interest of pathogenic mycobacteria, such as *Mycobacterium tuberculosis*, that have no counterpart in the corresponding non-pathogenic strains, such as *Mycobacterium bovis* BCG, and useful to detect the presence of polynucleotides belonging to a specific mycobacterium strain in a biological sample.

[015] By a biological sample according to the present invention, it is notably intended a biological fluid, such as plasma, blood, urine or saliva, or a tissue, such as a biopsy.

[016] Thus, a first object of the invention consists of a method for isolating a polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and that is absent or altered in the genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone belonging to a genomic DNA library of a given mycobacterium strain, said DNA library being cloned in a bacterial artificial chromosome (BAC).

[017] The invention is also directed to a polynucleotide of interest that has been isolated according to the above method and in particular a polynucleotide containing one or several Open Reading Frames (ORFs), for example ORFs encoding either a polypeptide involved in the pathogenicity of a mycobacterium strain or ORFs encoding Polymorphic Glycine Rich Sequences (PGRS).

[018] Such polynucleotides of interest may serve as probes or primers in order to detect the presence of a specific mycobacterium strain in a biological sample or to detect the expression of specific genes in a particular mycobacterial strain of interest.

[019] The BAC-based genomic mycobacterial DNA libraries generated by the present inventors are also part of the invention, as well as each of the recombinant BAC clones and the DNA insert contained in each of said recombinant BAC clones.

[020] The invention also pertains to methods and kits for detecting a specific mycobacterium in a biological sample using either at least one recombinant BAC clone or at least one polynucleotide according to the invention, as well as to methods and kits to detect the expression of one or several specific genes of a given mycobacterial strain present in a biological sample.

III. Brief description of the Figures.

[021] In order to better understand the present invention, reference will be made to the appended figures which depicted specific embodiments to which the present invention is in no case limited in scope with.

[022] **Figures 1A and 1B :** PCR-screening for unique BAC clones with specific primers for 2 selected genomic regions of the H37Rv chromosome, using 21 pools representating 2016 BACs (Figure 1A) and sets of 20 subpools from selected positive pools (Figure 1B).

[023] **Figure 2 :** Pulsed-field gel electrophoresis gel of *DraI*-cleaved BAC clones used for estimating the insert sizes of BACs.

[024] **Figure 3 :** Minimal overlapping BAC map of *M. tuberculosis* H37Rv superimposed on the integrated physical and genetic map established by Philipp et al. (18). Y- and I- numbers show pYUB328 (2) and pYUB412 (16) cosmids which were shotgun sequenced during the H37Rv genome sequencing project. Y-cosmids marked with * were shown in the integrated physical and genetic map (18). Rv numbers show the position of representative BAC clones relative to sequenced Y- and I- clones. Squared Rv numbers show BACs which were shotgun sequenced at the Sanger Centre.

[025] **Figures 4A and 4B :** Ethidium bromide stained gel (Figure 4A) and corresponding Southern blot (Figure 4B) of *EcoRI* and *PvuII* digested Rv58 DNA hybridized with ³²P labeled genomic DNA preparations from *M. tuberculosis* H37Rv, *M. bovis* ATCC 19210 and *M. bovis* BCG Pasteur.

[026] **Figure 5 :** Organisation of the ORFs in the 12.7 kb genomic region present in *M. tuberculosis* H37Rv but not present in *M. bovis* ATCC 19210 and *M. bovis* BCG

Pasteur. Arrows show the direction of transcription of the putative genes. Positions of *EcoRI* and *PvuII* restriction sites are shown. Vertical dashes represent stop codons. The 11 ORFs correspond to the ORFs MTCY277.28 to MTCY277.38 / accession number Z79701 -EMBL Nucleotide Sequence Data Library. The junction sequences flanking the polymorphic region are shown.

[027] **Figure 6** : Variation in the C-terminal part of a PE-PGRS open reading frame in *M. tuberculosis* strain H37Rv relative to *M. bovis* BCG strain Pasteur.

[028] The numbers on the right side of the Figure denote the position of the end nucleotides, taking as the reference the *M. tuberculosis* genome.

[029] **Figure 7** : Polynucleotide sequence next to the HindIII cloning site in the BAC vector pBeloBAC11 (Kim et al., 1996) used to clone the inserts of the BAC-based myobacterial genomic DNA library according to the invention.

[030] NotI : location of the NotI restriction sites.

[031] Primer T7-BAC1 : nucleotide region recognized by the T7-BAC1 primer shown in Table 1.

[032] T7 promoter: location of the T7 promoter region on the pBeloBac11 vector.

[033] Primer T7-Belo2 : nucleotide region recognized by the T7-Belo2 primer shown in Table 1.

[034] Hind III : the HindIII cloning site used to clone the genomic inserts in the pBeloBAC11 vector.

[035] SP6-Mid primer: nucleotide region recognized by the SP6 Mid primer shown in Table 1.

[036] SP6-BAC1 primer : nucleotide region recognized by the SP6 BAC1 primer shown in Table 1.

[037] SP6 promoter: location of the SP6 promoter region on the pBeloBac11 vector.

IV. Detailed description of the preferred embodiments.

[038] As already mentioned hereinbefore, the present invention is directed to a method for isolating a polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and that is absent or altered in the genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone

belonging to a genomic DNA library of a given mycobacterium strain, said DNA library being cloned in a bacterial artificial chromosome (BAC) type vector.

[039] For this purpose, the inventors have constructed several BAC-based mycobacterial genomic DNA libraries that may be used in order to perform the above described method.

[040] Because it is the first time that mycobacterial genomic, DNA has been successfully cloned in BAC type vectors, and because these DNA libraries are then novel and nonobvious, an object of the present invention consists in a mycobacterial genomic DNA library cloned in such a BAC type vector.

[041] As an illustrative example, a BAC-based DNA library of *Mycobacterium tuberculosis* has been realized. Forty-seven cosmids chosen from the integrated map of the 4.4 Mb circular chromosome (Philipp et al., 1996a) were shotgun-sequenced during the initial phase of the H37Rv genome sequence project. The sequences of these clones were used as landmarks in the construction of a minimally overlapping BAC map. Comparison of the sequence data from the termini of 420 BAC clones allowed us to establish a minimal overlapping BAC map and to fill in the existing gaps between the sequence of cosmids. As well as using the BAC library for genomic mapping and sequencing, we also tested the system in comparative genomic experiments in order to uncover differences between two closely related mycobacterial species. As shown in a previous study (Philipp et al., 1996b), *M. tuberculosis*, *M. bovis* and *M. bovis* BCG, specifically BCG Pasteur strain, exhibit a high level of global genomic conservation, but certain polymorphic regions were also detected. Therefore, it was of great interest to find a reliable, easy and rapid way to exactly localize polymorphic regions in mycobacterial genomes using selected BAC clones. This approach was validated by determining the exact size and location of the polymorphisms in the genomic region of *DraI* fragment Z4 (Philipp et al., 1996b), taking advantage of the availability of an appropriate BAC clone covering the polymorphic region and the H37Rv genome sequence data. This region is located approximately 1.7 Mb from the origin of replication.

[042] The Bacterial Artificial Chromosome (BAC) cloning system is capable of stably propagating large, complex DNA inserts in *Escherichia coli*. As part of the *Mycobacterium tuberculosis* H37Rv genome sequencing project, a BAC library was constructed in the pBeloBAC11 vector and used for genome mapping, confirmation of sequence assembly, and sequencing. The library contains about 5000 BAC clones, with inserts ranging in size from 25 to 104 kb, representing theoretically a 70 fold coverage of

the *M. tuberculosis* genome (4.4 Mb). A total of 840 sequences from the T7 and SP6 termini of 420 BACs were determined and compared to those of a partial genomic database. These sequences showed excellent correlation between the estimated sizes and positions of the BAC clones and the sizes and positions of previously sequenced cosmids and the resulting contigs. Many BAC clones represent linking clones between sequenced cosmids, allowing full coverage of the H37Rv chromosome, and they are now being shotgun-sequenced in the framework of the H37Rv sequencing project. Also, no chimeric, deleted or rearranged BAC clones were detected, which was of major importance for the correct mapping and assembly of the H37Rv sequence. The minimal overlapping set contains 68 unique BAC clones and spans the whole H37Rv chromosome with the exception of a single gap of ~ 150 kb. As a post-genomic application, the canonical BAC set was used in a comparative study to reveal chromosomal polymorphisms between *M. tuberculosis*, *M. bovis* and *M. bovis* BCG Pasteur, and a novel 12.7 kb segment present *M. tuberculosis* but absent from *M. bovis* and *M. bovis* BCG was characterized. This region contains a set of genes whose products show low similarity to proteins involved in polysaccharide biosynthesis. The H37Rv BAC library therefore provides the one skilled in the art with a powerful tool both for the generation and confirmation of sequence data as well as for comparative genomics and a plurality of post-genomic applications.

[043] The above described BAC-based *Mycobacterium tuberculosis* genomic DNA library is part of the present invention and has been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on November 19, 1997 under the accession number 1-1945.

[044] Another BAC-based DNA library has been constructed with the genomic DNA of *Mycobacterium bovis* BCG, Pasteur strain, and said DNA library has been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on June 30, 1998 under the accession number I-2049.

[045] Thus, as a specific embodiment of the above described method for isolating a polynucleotide of interest said method makes use of at least one BAC-based DNA library that has been constructed from the genomic DNA of *Mycobacterium tuberculosis*, more specifically of the H37Rv strain and particularly of the DNA library deposited in the accession number 1-1945.

[046] In another specific embodiment of the above described method for isolating a polynucleotide of interest said method makes use of at least one BAC-based

DNA library has been constructed from the genomic DNA of *Mycobacterium bovis* BCG, more specifically of the Pasteur strain and particularly of the DNA library deposited in the accession number I-2049.

[047] In more details, the method according to the invention for isolating a polynucleotide of interest may comprise the following steps :

[048] a) isolating at least one polynucleotide contained in a clone of a BAC-based DNA library of mycobacterial origin;

[049] b) isolating:

[050] - at least one genomic or cDNA polynucleotide from a mycobacterium, said mycobacterium belonging to a strain different from the strain used to construct the BAC-based DNA library of step a); or alternatively

[051] - at least one polynucleotide contained in a clone of a BAC-based DNA library prepared from the genome of a mycobacterium that is different from the mycobacterium used to construct the BAC-based DNA library of step a);

[052] c) hybridizing the at least one polynucleotide of step a) to the at least one polynucleotide of step b);

[053] d) selecting the at least one polynucleotide of step a) that has not formed a hybrid complex with the at least one polynucleotide of step b);

[054] e) characterizing the selected polynucleotide.

[055] Following the above procedure, the at least one polynucleotide of step a) may be prepared as follows :

[056] 1) digesting at least one recombinant BAC clone by an appropriate restriction endonuclease in order to isolate the polynucleotide insert of interest from the vector genetic material;

[057] 2) optionally amplifying the resulting polynucleotide insert;

[058] 3) optionally digesting the polynucleotide insert of step 1) or step 2) with at least one restriction endonuclease.

[059] The above method of the invention allows the one skilled in the art to perform comparative genomics between different strains or species of mycobacteria cells, for example between pathogenic strains or species and their non pathogenic strains or species counterparts, as it is the illustrative case for the genomic comparison between *Mycobacterium tuberculosis* and *Mycobacterium bovis* BCG that is described herein in the examples.

[060] Restriction digests of a given clone of a BAC library according to the invention may be blotted to membranes, and then probed with radiolabeled DNA from another strain or another species of mycobacteria, allowing the one skilled in the art to identify, characterize and isolate a polynucleotide of interest that may be involved in important metabolic and/or physiological pathways of the mycobacterium under testing, such as a polynucleotide functionally involved in the pathogenicity of said given mycobacteria for its host organism.

[061] More specifically, the inventors have shown in Example 6 that when restriction digests of a given clone of the BAC library identified by the CNCM accession number 1-1945 are blotted to membranes and then probed with radiolabeled total genomic DNA from, for example, *Mycobacterium bovis* BCG Pasteur, it is observed that restriction fragments that fail to hybridize with the *M. bovis* BCG Pasteur DNA are absent from its genome, hence identifying polymorphic regions between *M. bovis* BCG Pasteur and *M. tuberculosis* H37Rv.

[062] Thus, a further object of the present invention consists in a polynucleotide of interest that has been isolated according to the method described herein before.

[063] In Example 6, a polynucleotide of approximately 12.7 kilobases has been isolated that is present in the genome of *M. tuberculosis* but is absent of the genome of *M. bovis* BCG. This polynucleotide of interest contains 11 ORFs that may be involved in polysaccharide biosynthesis. In particular, two of said ORFs are of particular interest namely ORF6 (MTCY277.33; Rv1511) that encodes a protein that shares significant homology with bacterial GDP-D-mannose dehydratases, whereas the protein encoded by ORF7 (MTCY277.34; Rv1512) shares significant homology with a nucleotide sugar epimerase. As polysaccharide is a major constituent of the mycobacterial cell wall, these deleted genes may cause the cell wall of *M. bovis* BCG to differ from that of *M. tuberculosis*, a fact that may have important consequences for both the immune response to *M. bovis* BCG and virulence. Detection of such a polysaccharide is of diagnostic interest and possibly useful in the design of tuberculosis vaccines.

[064] Consequently, the polynucleotide of interest obtained following the method according to the invention may contain at least one ORF, said ORF preferably encoding all or part of a polypeptide involved in an important metabolic and/or physiological pathway of the mycobacteria under testing, and more specifically all or part of a polypeptide that is involved in the pathogenicity of the mycobacteria under testing,

such as for example *Mycobacterium tuberculosis*, and more generally mycobacteria belonging to the *Mycobacterium tuberculosis* complex.

[065] The *Mycobacterium tuberculosis* complex has its usual meaning, i.e. the complex of mycobacteria causing tuberculosis which are *Mycobacterium tuberculosis*, *Mycobacterium bovis*, *Mycobacterium africanum*, *Mycobacterium microti* and the vaccine strain *Mycobacterium bovis* BCG.

[066] An illustrative polynucleotide of interest according to the present invention comprises all or part of the polynucleotide of approximately 12.7 kilobases that is present in the genome of *M. tuberculosis* but is absent from the genome of *M. bovis* BCG disclosed hereinbefore. This polynucleotide is contained in clone Rv58 of the BAC DNA library I-1945.

[067] Generally, the invention also pertains to a purified polynucleotide comprising the DNA insert contained in a recombinant BAC vector belonging to a BAC-based mycobacterial genomic DNA library, such as for example the I-1945 BAC DNA library.

[068] Advantageously, such a polynucleotide has been identified according to the method of the invention.

[069] Such a polynucleotide of interest may be used as a probe or a primer useful for specifically detecting a given mycobacterium of interest, such as *Mycobacterium tuberculosis* or *Mycobacterium bovis* BCG.

[070] More specifically, the invention then deals with a purified polynucleotide useful as probe or a primer comprising all or part of the nucleotide sequence SEQ ID N° 1.

[071] The location, on the *Mycobacterium tuberculosis* chromosome, of the above polynucleotide of sequence SEQ ID N° 1 has now been ascribed to begin, at its 5' end at nucleotide at position nt 1696015 and to end, at its 3' end, at nucleotide at position nt 1708746.

[072] For diagnostic purposes, this 12.7 kb deletion should allow a rapid PCR screening of tubercle isolates to identify whether they are bovine or human strains. The primers listed in Table I are flanking the deleted region and give a 722 bp amplicon in *M. bovis* or *M. bovis* BCG strains, but a fragment of 13,453 bp in *M. tuberculosis* that is practically impossible to amplify under the same PCR conditions. More importantly, assuming that some of the gene products from this region represent proteins with antigenic properties, it could be possible to develop a test that can reliably distinguish

between the immune response induced by vaccination with *M. bovis* BCG vaccine strains and infection with *M. tuberculosis* or that the products (e.g. polysaccharides) are specific immunogens.

[073] The invention also provides for a purified polynucleotide useful as a probe or as a primer, said polynucleotide being chosen in the following group of polynucleotides :

[074] a) a polynucleotide comprising at least 8 consecutive nucleotides of the sequence SEQ ID N° 1;

[075] b) a polynucleotide whose sequence is fully complementary to the sequence of the polynucleotide defined in a);

[076] c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).

[077] For the purpose of defining a polynucleotide or oligonucleotide hybridizing under stringent hybridization conditions, such as above, it is intended a polynucleotide that hybridizes with a reference polynucleotide under the following hybridization conditions.

[078] The hybridization step is realized at 65°C in the presence of 6 x SSC buffer, 5 x Denhardt's solution, 0,5% SDS and 100µg/ml of salmon sperm DNA.

[079] For technical information, 1 x SSC corresponds to 0.15 M NaCl and 0.05M sodium citrate; 1 x Denhardt's solution corresponds to 0.02% Ficoll, 0.02% polyvinylpyrrolidone and 0.02% bovine serum albumin.

[080] The hybridization step is followed by four washing steps :

[081] - two washings during 5 min, preferably at 65°C in a 2 x SSC and 0.1% SDS buffer,

[082] - one washing during 30 min, preferably at 65°C in a 2 x SSC and 0.1% SDS buffer,

[083] - one washing during 10 min, preferably at 65°C in a 0.1 x SSC and 0.1%SDS buffer.

[084] A first illustrative useful polynucleotide that is included in the polynucleotide of sequence SEQ ID N°1 is the polynucleotide of sequence SEQ ID N°2 that corresponds to the Sp6 end-sequence of SEQ ID N°1.

[085] A second illustrative useful polynucleotide that is included in the polynucleotide of sequence SEQ ID N°1 is the polynucleotide of sequence SEQ ID N°3 that corresponds to the T7 end-sequence of SEQ ID N°1, located on the opposite strand.

[086] The polynucleotide of sequence SEQ ID N°1 contains 11 ORFs, the respective locations of which, taking into account the orientation of each ORF on the chromosome, on the sequence of the *Mycobacterium tuberculosis* chromosome, is given hereafter:

[087] - The location of ORF1 is comprised between nucleotide at position nt 1695944 and nucleotide at position nt 1696441.

[088] - The location of ORF2 is comprised between nucleotide at position nt 1696728 and nucleotide at position nt 1697420.

[089] - The location of ORF3 is comprised between nucleotide at position nt 1698096 and nucleotide at position nt 1699892. ORF3 probably encodes a protein having the characteristics of a membrane protein.

[090] - The location of ORF4 is comprised between nucleotide at position nt 1700210 and nucleotide at position nt 1701088.

[091] - The location of ORF5 is comprised between nucleotide at position nt 1701293 and nucleotide at position nt 1702588. ORF5 encodes a protein having the characteristics of a membrane protein.

[092] - The location of ORF6 is comprised between nucleotide at position nt 1703072 and nucleotide at position nt 1704091. ORF6 encodes a protein having the characteristics of a GDP-D-mannose dehydratase.

[093] - The location of ORF7 is comprised between nucleotide at position nt 1704091 and nucleotide at position nt 1705056. ORF7 encodes a protein having the characteristics of a nucleotide sugar epimerase involved in colanic acid biosynthesis.

[094] - The location of ORF8 is comprised between nucleotide at position nt 1705056 and nucleotide at position nt 1705784.

[095] - The location of ORF9 is comprised between nucleotide at position nt 1705808 and nucleotide at position nt 1706593. ORF9 encodes a protein having the characteristics of colanic acid biosynthesis glycosyl transferase.

[096] - The location of ORF10 is comprised between nucleotide at position nt 1706631 and nucleotide at position nt 1707524.

[097] - The location of ORF11 is comprised between nucleotide at position nt 1707530 and nucleotide at position nt1708648. ORF11 encodes a protein similar to a spore coat polysaccharide biosynthesis.

[098] A polynucleotide of interest obtained by the above-disclosed method according to the invention may also contain at least one ORF that encodes all or part of acidic, glycine-rich proteins, belonging to the PE and PPE families, whose genes are often clustered and based on multiple copies of the polymorphic repetitive sequences. The names PE and PPE derive from the fact that the motifs ProGlu (PE, positions 8, 9) and ProProGlu (PPE, positions 7 to 9) are found near the N-terminus in almost all cases. The PE protein family all have a highly conserved N-terminal domain of ~110 amino acid residues, that is predicted to have a globular structure, followed by a C-terminal segment which varies in size, sequence and repeat copy number. Phylogenetic analysis separated the PE family into several groups, the larger of which is the highly repetitive PGRS class containing 55 members whereas the other groups share very limited sequence similarity in their C-terminal domains. The predicted molecular weights of the PE proteins vary considerably as a few members only contain the ~110 amino acid N-terminal domain while the majority have C-terminal extensions ranging in size from 100 up to >1400 residues. A striking feature of the PGRS proteins is their exceptional glycine content (up to 50%) due to the presence of multiple tandem repetitions of GlyGlyAla or GlyGlyAsn motifs or variations thereof.

[099] Like the PE family, the PPE protein family also has a conserved N-terminal domain that comprises ~180 amino acid residues followed by C-terminal segments that vary considerably in sequence and length. These proteins fall into at least three groups, one of which constitutes the MPTR class characterised by the presence of multiple, tandem copies of the motif AsnXGlyXGlyAsnXGly (SEQ ID NO. 730). The second subgroup contains a characteristic, well-conserved motif around position 350 (GlyXXSerValProXXTrp)(SEQ ID NO. 731), whereas the other group contains proteins that are unrelated except for the presence of the common 180-residue PPE domain. C-terminal extensions may range in size from 00 up to 3500 residues.

[0100] One member of the PGRS sub-family, the WHO antigen 22T (Abou-Zeid et al., 1991), a 55kD protein capable of binding fibronectin, is produced during disease and elicits a variable antibody response suggesting either that individuals mount different immune responses or that this PGRS-protein may not be produced in this form by all strains of *M. tuberculosis*. In other words, at least some PE_PGRS coding sequences

encode for proteins that are involved in the recognition of *M. tuberculosis* by the immune system of the infected host. Therefore, differences in the PGRS sequences could represent the principal source of antigenic variation in the otherwise genetically and antigenically homogeneous bacterium.

[0101] By performing the method of the invention using the *M. tuberculosis* BAC based DNA library I-1945, the inventors have discovered the occurrence of sequence differences between a given PGRS encoding ORF (ORF reference on the genomic sequence of *M. tuberculosis* Rv0746) of *M. tuberculosis* and its counterpart sequence in the genome of *M. bovis* BCG.

[0102] More precisely, the inventors have determined that one ORF contained in BAC vector N° Rv418 of the *M. tuberculosis* BCG I-1945 DNA library carries both base additions and base deletions when compared with the corresponding ORF in the genome of *M. bovis* BCG that is contained in the BAC vector N° X0175 of the *M. bovis* BCG I-2049 DNA library. The variations observed in the base sequences correspond to variations in the C-terminal part of the aminoacid sequence of the PGRS ORF translation product.

[0103] As shown in Figure 6, an amino acid stretch of 9 residues in length is present in this *M. tuberculosis* PGRS (ORf reference Rv0746) and is absent from the ORF counterpart of *M. bovis* BCG, namely the following amino acid sequence:

[0104] NH₂-GGAGGAGGSSAGGGGAGGAGGAGGWLLGD-COOH (SEQ ID NO. 732).

[0105] Furthermore, Figure 6 shows also that an amino acid stretch of 45 residues in length is absent from this *M. tuberculosis* PGRS and is present in the ORF counterpart of *M. bovis* BCG, namely following amino acid sequence:

[0106] NH₂-GAGGIGGIGGNANGGAGGNGGTGGQLWGSGGAGVEGGAAL SVGDT-COOH (SEQ ID NO. 733).

[0107] Similar observations were made with PPE ORF Rv0442, which showed a 5 codon deletion relative to a *M. bovis* amino acid sequence.

[0108] Given that the polymorphism associated with the PE-PGRS or PEE ORFS resulted in extensive antigenic variability or reduced antigen presentation, this would be of immense significance for vaccine design, for understanding protective immunity in tuberculosis and, possibly, explain the varied responses seen in different BCG vaccination programmes.

[0109] There are several striking parallels between the PGRS proteins and the Epstein-Barr virus-encoded nuclear antigens (EBNA). Both polypeptide families are

glycine-rich, contain Gly-Ala repeats that represent more than one third of the molecule, and display variation in the length of the repeat region between different isolates. The Gly-Ala repeat region of EBNA1 has been shown to function as a *cis*-acting inhibitor of antigen processing and MHC class I-restricted antigen presentation. (Levitskaya et al., 1995). The fact that MHC class I knock-out mice are extremely susceptible to *M. tuberculosis* underlines the importance of MHC class I antigen presentation in protection against tuberculosis. Therefore, it is possible that the PE/PPE protein family also play some role in inhibiting antigen presentation, allowing the bacillus to hide from the host's immune system.

[0110] As such the novel and nonobvious PGRS polynucleotide from *M. bovis* which is homolog to the *M. tuberculosis* ORF Rv0746, and which is contained in the BAC clone N° X0175 (See Table 4 for SP6 and T7 end-sequences of clone n° X0175) of the I-2049 *M. bovis* BCG BAC DNA library is part of the present invention, as it represents a starting material in order to define specific probes or primers useful for detection of antigenic variability in mycobacterial strains, possible inhibition of antigen processing as well as to differentiate *M. tuberculosis* from *M. bovis* BCG.

[0111] Thus, a further object of the invention consists in a polynucleotide comprising the sequence SEQ ID N°4.

[0112] Polynucleotides of interest have been defined by the inventors as useful detection tools in order to differentiate *M. tuberculosis* from *M. bovis* BCG. Such polynucleotides are contained in the 45 aminoacid length coding sequence that is present in *M. bovis* BCG but absent from *M. tuberculosis*. This polynucleotide has a sequence beginning (5' end) at the nucleotide at position nt 729 of the sequence SEQ ID N°4 and ending (3' end) at the nucleotide in position nt 863 of the sequence SEQ ID N°4.

[0113] Thus, part of the present invention is also a polynucleotide which is chosen among the following group of polynucleotides :

[0114] a) a polynucleotide comprising at least 8 consecutive nucleotides of the nucleotide sequence SEQ ID N°5 ;

[0115] b) a polynucleotide which sequence is fully complementary to the sequence of the polynucleotide defined in a) ;

[0116] c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).

[0117] The stringent hybridization conditions for the purpose of defining the above disclosed polynucleotide are defined herein before in the specification.

[0118] The invention also provides for a BAC-based *Mycobacterium tuberculosis* strain H37Rv genomic DNA library that has been deposited in the Collection Nationale de Cultures de Microorganismes on November 19, 1997 under the accession number I-1945.

[0119] A further object of the invention consists in a recombinant BAC vector which is chosen among the group consisting of the recombinant BAC vectors belonging to the BAC-based DNA library I-1945.

[0120] Generally, a recombinant BAC vector of interest may be chosen among the following set or group of BAC vectors contained in the BAC-based DNA library I-1945 :

[0121] Rv101; Rv102; Rv103; Rv104; Rv105; Rv106; Rv107; Rv108; Rv109; Rv110; Rv111; Rv112; Rv113; Rv114; Rv115; Rv116; Rv117; Rv118; Rv119; Rv120; Rv121; Rv122; Rv123; Rv124; Rv126; Rv127; Rv128; Rv129; Rv130; Rv132; Rv134; Rv135; Rv136; Rv137; Rv138; Rv139; Rv140; Rv141; Rv142; Rv143; Rv144; Rv145; Rv146; Rv147; Rv148; Rv149; Rv150; Rv151; Rv152; Rv153; Rv154; Rv155; Rv156; Rv157; Rv159; Rv160; Rv161; Rv162; Rv163; Rv164; Rv165; Rv166; Rv167; Rv169; Rv170; Rv171; Rv172; Rv173; Rv174; Rv175; Rv176; Rv177; Rv178; Rv179; Rv180; Rv181; Rv182; Rv183; Rv184; Rv185; Rv186; Rv187; Rv188; Rv189; Rv190; Rv191; Rv192; Rv193; Rv194; Rv195; Rv196; Rv197; Rv198; Rv199; Rv200; Rv201; Rv204; Rv205; Rv207; Rv209; Rv210; Rv214; Rv215; Rv217; Rv218; Rv219; Rv220; Rv221; Rv222; Rv223; Rv224; Rv225; Rv226; Rv227; Rv228; Rv229; Rv230; Rv231; Rv232; Rv233; Rv234; Rv235; Rv237; Rv240; Rv241; Rv243; Rv244; Rv245; Rv246; Rv247; Rv249; Rv250; Rv251; Rv252; Rv253; Rv254; Rv255; Rv257; Rv258; Rv259; Rv260; Rv261; Rv262; Rv263; Rv264; Rv265; Rv266; Rv267; Rv268; Rv269; Rv270; Rv271; Rv272; Rv273; Rv274; Rv275; Rv276; Rv277; Rv278; Rv279; Rv280; Rv281; Rv282; Rv283; Rv284; Rv285; Rv286; Rv287; Rv288; Rv289; Rv290; Rv291; Rv292; Rv293; Rv294; Rv295; Rv296; Rv297; Rv298; Rv299; Rv300; Rv301; Rv302; Rv303; Rv304; Rv306; Rv307; Rv308; Rv309; Rv310; Rv311; Rv312; Rv313; Rv314; Rv315; Rv316; Rv317; Rv318; Rv319; Rv320; Rv321; Rv322; Rv327; Rv328; Rv329; Rv330; Rv331; Rv333; Rv334; Rv335; Rv336; Rv337; Rv338; Rv339; Rv340; Rv341; Rv343; Rv344; Rv346; Rv347; Rv348; Rv349; Rv350; Rv351; Rv352; Rv353; Rv354; Rv355; Rv356; Rv357; Rv358; Rv359; Rv360; Rv361; Rv363; Rv364; Rv365; Rv366; Rv367; Rv368; Rv369; Rv370; Rv371; Rv373; Rv374; Rv375; Rv376; Rv377; Rv378; Rv379; Rv380; Rv381; Rv382; Rv383; Rv384; Rv385; Rv386; Rv387; Rv388;

Rv389; Rv38; Rv390; Rv391; Rv392; Rv393; Rv396; Rv39; Rv3; Rv40; Rv412; Rv413; Rv414; Rv415; Rv416; Rv417; Rv418; Rv419; Rv41; Rv42; Rv43; Rv44; Rv45; Rv46; Rv47; Rv48; Rv49; Rv4; Rv50; Rv51; Rv52; Rv53; Rv54; Rv55; Rv56; Rv57; Rv58; Rv59; Rv5; Rv60; Rv61; Rv62; Rv63; Rv64; Rv65; Rv66; Rv67; Rv68; Rv69; Rv6; Rv70; Rv71; Rv72; Rv73; Rv74; Rv75; Rv76; Rv77; Rv78; Rv79; Rv7; Rv80; Rv81; Rv82; Rv83; Rv84; Rv85; Rv86; Rv87; Rv88; Rv89; Rv8; Rv90; Rv91; Rv92; Rv94; Rv95; Rv96; Rv9.

[0122] The end sequences of the polynucleotide inserts of each of the above clones corresponding respectively to the sequences adjacent to the T7 promoter and to the Sp6 promoter on the BAC vector are shown in Table 3.

[0123] It has been shown by the inventors that the minimal overlapping set of BAC vectors of the BAC-based DNA library I-1945 contains 68 unique BAC clones and practically spans almost the whole H37Rv chromosome with the exception of a single gap of approximately 150 kb.

[0124] More specifically, a recombinant BAC vector of interest is chosen among the following set or group of BAC vectors from the BAC-based DNA library I-1945, the location of which vector DNA inserts on the chromosome of *M. tuberculosis* is shown in Figure 3 :

[0125] Rv234; Rv351; Rv166; Rv35; Rv415; Rv404; Rv209; Rv272; Rv30; Rv228; Rv233; Rb38; Rv280; Rv177; Rv48; Rv374; Rv151; Rv238; Rv156; Rv92; Rv3; Rv403; Rv322; Rv243; Rv330; Rv285; Rv233; Rv219; Rv416; Rv67; Rv222; Rv149; Rv279; Rv87; Rv273; Rv266; Rv25; Rv136; Rv414; Rv13; Rv289; Rv60; Rv104; Rv5; Rv165; Rv215; Rv329; Rv240; Rv19; Rv74; Rv411; Rv167; Rv56; Rv80; Rv164; Rv59; Rv313; Rv265; Rv308; Rv220; Rv258; Rv339; Rv121; Rv419; Rv418; Rv45; Rv217; Rv134; Rv17; Rv103; Rv21; Rv22; Rv2; Rv270; Rv267; Rv174; Rv257; Rv44; Rv71; Rv7; Rv27; Rv191; Rv230; Rv128; Rv407; Rv106; Rv39; Rv255; Rv74; Rv355; Rv268; Rv58; Rv173; Rv264; Rv417; Rv401; Rv144; Rv302; Rv81; Rv163; Rv281; Rv221; Rv420; Rv175; Rv86; Rv412; Rv73; Rv269; Rv214; Rv287; Rv42; Rv143.

[0126] The polynucleotides disclosed in Table 3 may be used as probes in order to select a given clone of the BAC DNA library I-1945 for further use.

[0127] The invention also provides for a BAC-based *Mycobacterium bovis* strain Pasteur genomic DNA library that has been deposited in the Collection Nationale de Cultures de Microorganismes on June 30, 1998 under the accession number I-2049.

[0128] A further object of the invention consists in a recombinant BAC vector which is chosen among the group consisting of the recombinant BAC vectors belonging to the BAC-based DNA library I-2049. This DNA library contains approximately 1600 clones. The average insert size is estimated to be ~80 kb.

[0129] Generally, a recombinant BAC vector of interest may be chosen among the following set or group of BAC vectors contained in the BAC-based DNA library I-2049:

[0130] X0001; X0002; X0003; X0004; X0006; X0007; X0008; X0009; X0010; X0012; X0013; X0014; X0015; X0016; X0017; X0018; X0019; X0020; X0021; X0175.

[0131] The end sequences of the polynucleotide inserts of each of the above clones corresponding respectively to the sequences adjacent to the T7 promoter and to the Sp6 promoter on the BAC vector are shown in Table 4.

[0132] The polynucleotides disclosed in Table 4 may be used as probes in order to select a given clone of the BAC DNA library I-2049 for further use.

[0133] Are also part of the invention the polynucleotide inserts that are contained in the above described BAC vectors, that are useful as primers or probes.

[0134] These polynucleotides and nucleic acid fragments may be used as primers for use in amplification reactions, or as nucleic probes.

[0135] PCR is described in the US patent N° 4,683,202. The amplified fragments may be identified by an agarose or a polyacrylamide gel electrophoresis, or by a capillary electrophoresis or alternatively by a chromatography technique (gel filtration, hydrophobic chromatography or ion exchange chromatography). The specificity of the amplification may be ensured by a molecular hybridization using, for example, one of the initial primers as nucleic probes.

[0136] Amplified nucleotide fragments are used as probes in hybridization reactions in order to detect the presence of one polynucleotide according to the present invention or in order to detect mutations in the genome of the given mycobacterium of interest, specifically a mycobacterium belonging to the *Mycobacterium tuberculosis* complex and more specifically *Mycobacterium tuberculosis* and *Mycobacterium bovis* BCG.

[0137] Are also part of the present invention the amplified nucleic fragments («amplicons») defined herein above.

[0138] These probes and amplicons may be radioactively or non-radioactively labeled, using for example enzymes or fluorescent compounds.

[0139] Other techniques related to nucleic acid amplification may also be used and are generally preferred to the PCR technique.

[0140] The Strand Displacement Amplification (SDA) technique (Walker et al., 1992) is an isothermal amplification technique based on the ability of a restriction enzyme to cleave one of the strands at his recognition site (which is under a hemiphosphorothioate form) and on the property of a DNA polymerase to initiate the synthesis of a new strand from the 3'OH end generated by the restriction enzyme and on the property of this DNA polymerase to displace the previously synthesized strand being localized downstream. The SDA method comprises two main steps:

[0141] a) The synthesis, in the presence of dCTP- α -S, of DNA molecules that are flanked by the restriction sites that may be cleaved by an appropriate enzyme.

[0142] b) The exponential amplification of these DNA molecules modified as such, by enzyme cleavage, strand displacement and copying of the displaced strands. The steps of cleavage, strand displacement and copy are repeated a sufficient number of times in order to obtain an accurate sensitivity of the assay.

[0143] The SDA technique was initially realized using the restriction endonuclease HincII but is now generally practised with an endonuclease from *Bacillus stearothermophilus* (BSOBI) and a fragment of a DNA polymerase which is devoid of any 5'→3'exonuclease activity isolated from *Bacillus cladothrix* (exo- Bca) [=exo-minus-Bca]. Both enzymes are able to operate at 60°C and the system is now optimized in order to allow the use of dUTP and the decontamination by UDG. When using this technique, as described by Spargo et al. in 1996, the doubling time of the target DNA is of 26 seconds and the amplification rate is of 10^{10} after an incubation time of 15 min at 60°C.

[0144] The SDA amplification technique is more easy to perform than PCR (a single thermostated waterbath device is necessary) and is faster than the other amplification methods.

[0145] Thus, another object of the present invention consists in using the nucleic acid fragments according to the invention (primers) in a method of DNA or RNA amplification according to the SDA technique. For performing SDA, two pairs of primers are used : a pair of external primers (B1, B2) consisting of a sequence specific for the target polynucleotide of interest and a pair of internal primers (S1, S2) consisting of a fusion oligonucleotide carrying a site that is recognized by a restriction endonuclease, for example the enzyme BSOBI.

[0146] The operating conditions to perform SDA with such primers are described in Spargo et al, 1996.

[0147] The polynucleotides of the invention and their above described fragments, especially the primers according to the invention, are useful as technical means for performing different target nucleic acid amplification methods such as:

[0148] - TAS (Transcription-based Amplification System), described by Kwoh et al. in 1989.

[0149] - SR (Self-Sustained Sequence Replication), described by Guatelli et al. in 1990.

[0150] - NASBA (Nucleic acid Sequence Based Amplification), described by Kievitis et al. in 1991.

[0151] - TMA (Transcription Mediated Amplification).

[0152] The polynucleotides according to the invention are also useful as technical means for performing methods for amplification or modification of a nucleic acid used as a probe, such as:

[0153] - LCR (Ligase Chain Reaction), described by Landegren et al. in 1988 and improved by Barany et al. in 1991 who employ a thermostable ligase.

[0154] - RCR (Repair Chain Reaction) described by Segev et al. in 1992.

[0155] - CPR (Cycling Probe Reaction), described by Duck et al. in 1990.

[0156] - Q-beta replicase reaction, described by Miele et al. in 1983 and improved by Chu et al. in 1986, Lizardi et al. in 1988 and by Burg et al. and Stone et al. in 1996.

[0157] When the target polynucleotide to be detected is a RNA, for example a mRNA, a reverse transcriptase enzyme will be used before the amplification reaction in order to obtain a cDNA from the RNA contained in the biological sample. The generated cDNA is subsequently used as the nucleic acid target for the primers or the probes used in an amplification process or a detection process according to the present invention.

[0158] The non-labeled polynucleotides or oligonucleotides of the invention may be directly used as probes. Nevertheless, the polynucleotides or oligonucleotides are generally labeled with a radioactive element (^{32}P , ^{35}S , ^3H , ^{125}I) or by a nonisotopic molecule (for example, biotin, acetylaminofluorene, digoxigenin, 5bromodesoxyuridin, fluorescein) in order to generate probes that are useful for numerous applications.

[0159] Examples of non-radioactive labeling, of nucleic acid -fragments are described in the french patent N° FR-7810975 or by Urdea et al. or Sanchez-Pescador et al., 1988.

[0160] In the latter case, other labeling techniques may be also used such as those described in the french patents FR-2 422 956 and 2 518 755. The hybridization step may be performed in different ways (Matthews et al., 1988). The more general method consists of immobilizing the nucleic acid that has been extracted from the biological sample onto a substrate (nitrocellulose, nylon, polystyrene) and then to incubate, in defined conditions, the target nucleic acid with the probe. Subsequently to the hybridization step, the excess amount of the specific probe is discarded and the hybrid molecules formed are detected by an appropriate method (radioactivity, fluorescence or enzyme activity measurement).

[0161] Advantageously, the probes according to the present invention may have structural characteristics such that they allow the signal amplification, such structural characteristics being, for example, branched DNA probes as those described by Urdea et al. in 1991 or in the European patent N° EP-0 225 807 (Chiron).

[0162] In another advantageous embodiment of the probes according to the present invention, the latters may be used as « capture probes », and are for this purpose immobilized on a substrate in order to capture the target nucleic acid contained in a biological sample. The captured target nucleic acid is subsequently detected with a second probe which recognizes a sequence of the target nucleic acid which is different from the sequence recognized by the capture probe.

[0163] The oligonucleotide probes according to the present invention may also be used in a detection device comprising a matrix library of probes immobilized on a substrate, the sequence of each probe of a given length being localized in a shift of one or several bases, one from the other, each probe of the matrix library thus being complementary to a distinct sequence of the target nucleic acid. Optionally, the substrate of the matrix may be a material able to act as an electron donor, the detection of the matrix poisitons in which an hybridization has occurred being subsequently determined by an electronic device. Such matrix libraries of probes and methods of specific detection of a targer nucleic acid is described in the European patent application N° EP-0 713 016 (Affymax technologies) and also in the US patent N° US-5,202,231 (Drmanac).

[0164] Since almost the whole length of a mycobacterial chromososome is covered by a BAC-based genomic DNA libraries according to the present invention (i.e. 97% of the *M. tuberculosis* chromosome is covered by the BAC library I-1945), these DNA libraries will play an important role in a plurality of post-genomic applications, such as in mycobacterial gene expression studies where the canonical set of BACs could be used as

a matrix for hybridization studies. Probing such matrices with cDNA probes prepared from total mRNA will uncover genetic loci induced or repressed under different physiological conditions (Chuang et al., 1993; Trieselmann et al., 1992). As such, the H37Rv BAC library represents a fundamental resource for present and future genomics investigations.

[0165] The BAC vectors or the polynucleotide inserts contained therein may be directly used as probes, for example when immobilized on a substrate such as described herein before.

[0166] The BAC vectors or their polynucleotide inserts may be directly adsorbed on a nitrocellulose membrane, at predetermined locations on which one or several polynucleotides to be tested are then put to hybridize therewith.

[0167] Preferably, a collection of BAC vectors that spans the whole genome of the mycobacterium under testing will be immobilized, such as, for example, the set of 68 BAC vectors of the I-1945 DNA library that is described elsewhere in the specification and shown in Figure 3.

[0168] The immobilization and hybridization steps may be performed as described in the present Materials and Methods Section.

[0169] As another illustrative embodiment of the use of the BAC vectors of the invention as polynucleotide probes, these vectors may be useful to perform a transcriptional activity analysis of mycobacteria growing in different environmental conditions, for example under conditions in which a stress response is expected, as it is the case at an elevated temperature, for example 40°C.

[0170] In this specific embodiment of the invention, Genescreen membranes may be used to immobilize the restriction endonuclease digests (*Hind*III digests for the BAC DNA library I-1945) of the BAC vectors by transfer from a gel (Trieselmann et al., 1992).

[0171] Alternatively, the BAC vectors may be immobilized for dot blot experiments as follows. First, the DNA concentration of each BAC clone is determined by hybridization of blots of clone DNAs and of a BAC vector concentration standard with a BAC vector specific DNA probe. Hybridization is quantified by the Betascope 603 blot analyzer (Betagen Corp.), which collects beta particles directly from the blot with high efficiency. Then, 0.5 µg of each clone DNA is incubated in 0.25 M NaOH and 10 mM EDTA at 65°C for 60 min to denature the DNA and degrade residual RNA contaminants. By using a manifold filtration system (21 by 21 wells), each clone DNA is blotted onto a GeneScreen Plus nylon membrane in the alkaline solution. After neutralization, the blots

are baked at 85°C for 2 h under vacuum. Positive and negative controls are added when necessary. In order to perform this procedure, it may be referred to the article of Chuang et al. (1993).

[0172] For RNA extractions, cells grown in a suitable volume of culture medium may, for example, be immediately mixed with an equal volume of crushed ice at -70°C and spun at 4°C in a 50 ml centrifugation tube. The cell pellet is then suspended in 0.6 ml of ice-cold buffer (10 mM KCl, 5 mM MgCl, 10 mM Tris; pH 7.4) and then immediately added to 0.6 ml of hot lysis buffer (0.4 M NaCl, 40 mM EDTA, 1% beta-mercaptoethanol, 1% SDS, 20 mM Tris; pH 7.4) containing 100 µl of water saturated phenol. This mixture is incubated in a boiling water bath for 40 s. The debris are removed by centrifugation. The supernatant is extracted with phenol-chloroform five times, ethanol precipitated, and dried. The dried RNA pellet is dissolved in water before use.

[0173] Then labeled total cDNA may be prepared by the following method. The reaction mixture contains 15 µg of the previously prepared total RNA, 5 µg of pd(N₆) (random hexamers from Pharmacia Inc.), 0.5 mM dATP, 0.5 mM dGTP and 0.5 mM DTTP, 5 µM dCTP, 100 µCi of [α -³²P]dCTP (3,000 Ci/mmol), 50 mM Tris-HCl (pH 8.3), 6 mM MgCl₂, 40 mM KCl, 0.5 U of avian myeloblastosis virus reverse transcriptase (Life Science Inc.) in a total volume of 50 µl. The reaction is allowed to continue overnight at room temperature. EDTA and NaOH are then added to final concentrations of 50 mM and 0.25 M, respectively, and the mixture is incubated at 65°C for 30 min to degrade the RNA templates. The cDNA is then ready to use after neutralization by adding HCl and Tris buffer.

[0174] The hybridization step may be performed as described by Chuang et al. (1993) and briefly disclosed hereinafter. The DNA dot blot is hybridized to ³²P- labeled total cDNA in a solution containing 0.1% polyvinylpyrrolidone, 0.1% Ficoll 0.1% sodium Ppi, 0.1% bovine serum albumin, 0.5% SDS, 100 mM NaCl, and 0.1 mM sodium citrate, pH 7.2, at 65°C for 2 days and then washed with a solution containing 0.1% SDS, 100 mM NaCl, and 10 mM Na-citrate, pH 7.2. The same dot blot is used for hybridization with both control and experimental cDNAs, with an alkaline probe stripping procedure (soaked twice in 0.25M NaOH-0.75 M NaCl at room temperature, 30 min each, neutralized, and completely dried at 65°C for at least 30 min) between the two hybridizations. Quantification may be done with the Betascope 603 blot analyzer (Betagen Corp.).

[0175] As it flows from the above technical teachings, another object of the invention consists in a method for detecting the presence of mycobacteria in a biological sample comprising the steps of:

[0176] a) bringing into contact the recombinant BAC vector or a purified polynucleotide according to the invention with a biological sample ;

[0177] b) detecting the hybrid nucleic acid molecule formed between said purified polynucleotide and the nucleic acid molecules contained within the biological sample.

[0178] The invention further deals with a method for detecting the presence of mycobacteria in a biological sample comprising the steps of:

[0179] a) bringing into contact the recombinant BAC vector or a purified polynucleotide according to the invention that has been immobilized onto a substrate with a biological sample;

[0180] b) bringing into contact the hybrid nucleic acid molecule formed between said purified polynucleotide and the nucleic acid contained in the biological sample with a labeled recombinant BAC vector or a polynucleotide according to the invention, provided that said polynucleotide and polynucleotide of step a) have non-overlapping sequences.

[0181] Another object of the invention consists in a method for detecting the presence of mycobacteria in a biological sample comprising the steps of:

[0182] a) bringing into contact the nucleic acid molecules contained in the biological sample with a pair of primers according to the invention;

[0183] b) amplifying said nucleic acid molecules;

[0184] c) detecting the nucleic acid fragments that have been amplified, for example by gel electrophoresis or with a labeled polynucleotide according to the invention.

[0185] In one specific embodiment of the above detection and/or amplification methods, said methods comprise an additional step wherein before step a), the nucleic acid molecules of the biological sample have been made available to a hybridization reaction.

[0186] In another specific embodiment of the above detection methods, said methods comprise an additional step, wherein, before the detection step, the nucleic acid molecules that are not hybridized with the immobilized purified polynucleotide are removed.

[0187] Also part of the invention is a kit for detecting mycobacteria in a biological sample comprising:

[0188] a) a recombinant BAC vector or a purified polynucleotide according to the invention;

[0189] b) reagents necessary to perform a nucleic acid hybridization reaction.

[0190] The invention also pertains to a kit for detecting a mycobacteria in a biological sample comprising:

[0191] a) a recombinant BAC vector or a purified polynucleotide according to the invention that is immobilized onto a substrate;

[0192] b) reagents necessary to perform a nucleic acid hybridization reaction;

[0193] c) a purified polynucleotide according to the invention which is radioactively or non-radioactively labeled, provided that said polynucleotide and the polynucleotide of step a) have non-overlapping sequences.

[0194] Moreover, the invention provides for a kit for detecting mycobacteria in a biological sample comprising:

[0195] a) a pair of purified primers according to the invention;

[0196] b) reagents necessary to perform a nucleic acid amplification reaction;

[0197] c) optionally, a purified polynucleotide according to the invention useful as a probe.

[0198] The invention embraces also a method for detecting the presence of a genomic DNA, a cDNA or a mRNA of mycobacteria in a biological sample, comprising the steps of :

[0199] a) bringing into contact the biological sample with a plurality of BAC vectors according to the invention or purified polynucleotides according to the invention, that are immobilized on a substrate;

[0200] b) detecting the hybrid complexes formed.

[0201] The invention also provides a kit for detecting the presence of genomic DNA, cDNA or mRNA of a mycobacterium in a biological sample, comprising:

[0202] a) a substrate on which a plurality of BAC vectors according to the invention or purified polynucleotides according to the invention have been immobilized;

[0203] b) optionally, the reagents necessary to perform the hybridization reaction.

[0204] Additionally, the recombinant BAC vectors according to the invention and the polynucleotide inserts contained therein may be used for performing detection methods based on « molecular combing ». Said methods consist in methods for aligning

macromolecules, especially DNA and are applied to processes for detecting, for measuring intramolecular distance, for separating and/or for assaying a macromolecule, especially DNA in a sample.

[0205] These « molecular combing » methods are simple methods, where the triple line S/A/B (meniscus) resulting from the contact between a solvent A and the surface S and a medium B is caused to move on the said surface S, the said macromolecules (i.e. DNA) having a part, especially an end, anchored on the surface S, the other part, especially the other end, being in solution in the solvent A. These methods are particularly fully described in the PCT Application n° PCT/FR 95/00165 filed on February 11, 1994 (Bensimon et al.).

[0206] When performing the « molecular combing » method with the recombinant BAC vectors according to the inventions or their polynucleotide inserts, the latter may be immobilized (« anchored ») on a suitable substrate and aligned as described in the PCT Application n° PCT/FR 95/00165, the whole teachings of this PCT Application being hereby incorporated by reference. Then, polynucleotides to be tested, preferably under the form of radioactively or non radioactively labeled polynucleotides, that may consist of fragments of genomic DNA, cDNA etc. are brought into contact with the previously aligned polynucleotides according to the present invention and then their hybridization position on the aligned DNA molecules is determined using any suitable means including a microscope or a suitable camera device.

[0207] Thus, the present invention is also directed to a method for the detection of the presence of a polynucleotide of mycobacterial origin in a biological sample and/or for physical mapping of a polynucleotide on a genomic DNA, said method comprising:

[0208] a) aligning at least one polynucleotide contained in a recombinant BAC vector according to the invention on the surface of a substrate;

[0209] b) bringing into contact at least one polynucleotide to be tested with the substrate on which the at least one polynucleotide of step a) has been aligned;

[0210] c) detecting the presence and/or the location of the tested polynucleotide on the at least one aligned polynucleotide of step a).

[0211] The invention finally provides for a kit for performing the above method, comprising:

[0212] a) a substrate whose surface has at least one polynucleotide contained in a recombinant BAC vector according to the invention;

[0213] b) optionally, reagents necessary for labeling DNA;

[0214] c) optionally, reagents necessary for performing a hybridization reaction.

[0215] In conclusion, it may be underlined that the alliance of such BAC-based approaches such as described in the present specification to the advances in comparative genomics by the availability of an increased number of complete genomes, and the rapid increase of well-characterized gene products in the public databases, will allow the one skilled in the art an exhaustive analysis of the mycobacterial genome.

MATERIALS AND METHODS

[0216] 1. DNA-preparation. Preparation of *M tuberculosis* H37Rv DNA in agarose plugs was conducted as previously described (Canard et al., 1989; Philipp et al., 1996b). Plugs were stored in 0.2 M EDTA at 4°C and washed 3 times in 0.1% Triton X-100 buffer prior to use.

[0217] 2. BAC vector preparation. pBeloBAC11 was kindly provided by Dr. Shizuya, Department of Biology, California Institute of Technology (Pasadena, CA). The preparation followed the description of Woo et al., 1994 (Woo et al., 1994).

[0218] 3. Partial digestion with *Hind*III. Partial digestion was carried out on plugs, each containing approximately 10 µg of high molecular weight DNA, after three one hour equilibration steps in 50 ml of *Hind*III 1X digestion buffer (Boehringer Mannheim, Mannheim, Germany) plus 0.1% Triton X-100. The buffer was then removed and replaced by 1ml/plug of ice-cold *Hind*III enzyme buffer containing 20 units of *Hind*III (Boehringer). After two hours incubation on ice, the plugs were transferred to a 37°C water bath for 30 minutes. Digestions were stopped by adding 500 µl of 50 mM EDTA (pH 8.0).

[0219] 4. Size selection. The partially digested DNA was subjected to contour-clamped homogenous electric field (CHEF) electrophoresis on a 1% agarose gel using a BioRad DR III apparatus (BioRad, Hercules, CA) in IX TAE buffer at 13°C, with a ramp from 3 to 15 seconds at 6 V/cm for 16 hours. Agarose slices from 25 to 75 kb, 75 to 120 kb and 120 to 180 kb were excised from the gel and stored in TE at 4°C.

[0220] 5. Ligation and transformation. Agarose-slices containing fractions from 25 to 75 kb, 75 to 120 kb and 120 to 180 kb were melted at 65°C for 10 minutes and digested with Gelase (Epicentre Technologies, Madison, WI), using 1 unit per 100 µl gel-slice. 25-100 ng of the size-selected DNA was then ligated to 10 ng of *Hind*III digested, dephosphorylated pBeloBAC11 in a 1:10 molar ratio using 10 units of T4 DNA ligase (New England Biolabs, Beverly, MA) at 16°C for 20 hours. Ligation mixtures were heated at 65°C for 15 minutes, then drop-dialysed against TE using Millipore VS 0.025

mM membranes (Millipore, Bedford, MA). Fresh electrocompetent *E. coli* DH10B cells (Sheng et al., 1995) were harvested from 200 ml of a mid-log ($OD_{550}=0.5$) culture grown in SOB medium. Cells were washed three times in ice-cold water, and finally resuspended in ice-cold water to a cell density of 10^{11} cells/ml ($OD_{550}=150$). 1 μ l of the ligation-mix was used for electroporation of 30 μ l of electrocompetent DH10B *E. coli* using a Eurogentec Easyject Plus electroporator (Eurogentec, Seraing, Belgium), with settings of 2.5 kV, 25 μ F, and 99 Ω , in 2 mm wide electroporation cuvettes. After electroporation, cells were resuspended in 600 μ l of SOC medium, allowed to recover for 45 minutes at 37°C with gentle shaking, and then plated on LB agar containing 12.5 μ g/ml chloramphenicol (CM), 50 μ g/ml-X-gal, and 25 μ g/ml IPTG. The plates were incubated overnight and recombinants (white colonies) were picked manually to 96 well plates. Each clone was inoculated 3 times (2 X 200 μ l and 1 X 100 μ l of 2YT/12.5 μ g/ml CM per clone) and incubated overnight. One of the microtiter plates, containing 100 μ l culture per well, was maintained as a master plate at -80°C after 100 μ l of 80% glycerol were added to each well, while minipreps (Sambrook et al., 1989) were prepared from the remaining two plates to check for the presence of inserts. Clones containing inserts were then designated "Rv" clones, repicked from the master plate to a second set of plates for storage of the library at -80°C.

[0221] 6. Preparation of DNA for sizing, direct sequencing and comparative genomics. A modified Birnboim and Doly protocol (Birnboim et al., 1979) was used for extraction of plasmid DNA for sequencing purposes. Each Rv clone was inoculated into a 50 ml Falcon polypropylene tube containing 40 ml of 2YT medium with 12.5 μ g/ml of CM and grown overnight at 37°C with shaking. Cells were harvested by centrifugation and stored at -20°C. The frozen pellet was resuspended in 4 ml of Solution A (50 mM glucose, 10 mM EDTA, 25 mM Tris, pH 8.0) and 4 ml of freshly prepared solution B (0.2 M NaOH 0.2% SDS) was then added. The solution was gently mixed and kept at room temperature for 5 minutes before adding 4 ml of ice-cold solution C (3M Sodium Acetate, pH 4.7). Tubes were kept on ice for 15 min, and centrifuged at 10,000 rpm for 15 min. After isopropanol precipitation, the DNA pellet was dissolved in 600 μ l RNase solution (15 mM Tris HCl pH 8.0, 10 μ g/ml RNase A). After 30 minutes at 37°C the DNA solution was extracted with chloroform:isoamylalcohol (24:1) and precipitated from the aqueous phase using isopropanol. The DNA pellet was then rinsed with 70% ethanol, air-dried and dissolved in 30 μ l distilled water. In general, DNA prepared by this method was clean and concentrated enough to give good quality results by automatic sequencing

(at least 300 bp of sequence). For a few DNA preparations, an additional polyethylene glycol (PEG) precipitation step was necessary, which was performed as follows. The 30 µl of DNA solution were diluted to 64µl, mixed gently and precipitated using 16 µl 4M NaCl and 80 µl of 13% PEG 8000. After 30 min on ice the tubes were centrifuged at 4°C, the pellet carefully rinsed with 70% ethanol, air-dried and diluted in 20 µl of distilled water.

[0222] 7. Sizing of inserts. Insert sizes were determined by pulsed-field gel electrophoresis (PFGE) after cleavage with *DraI* (Promega). 100-200 ng of DNA was *DraI*-cleaved in 20 µl total reaction volume, following the manufacturer's recommendations, then loaded onto a 1% agarose gel and migrated using a pulse of 4 s for 15 h at 6.25 V/cm at 10°C on an LKB-Pharmacia CHEF apparatus. Mid-range and low-range PFGE markers (New England Biolabs) were used as size standards. Insert sizes were estimated after ethidium bromide staining of gels.

[0223] 8. Direct sequencing. For each sequencing reaction 7 µl BAC DNA (300-500ng), 2 µl primer (2 µM), 8 µl reaction mix of the *Taq* DyeDeoxy Terminator cycle sequencing kit (Applied Biosystems) and 3 µl distilled water were used.

[0224] After 26 cycles (96°C for 30 sec; 56°C for 15 sec; 60°C for 4 min) in a thermocycler (MJ-research Inc., Watertown, MA) DNA was precipitated using 70 µl of 70% ethanol/0.5 mM MgCl₂, centrifuged, rinsed with 70% ethanol, dried and dissolved in 2 µl of formamide/EDTA buffer. SP6 and T7 samples of 32 BAC clones were loaded onto 64 lane, 6% polyacrylamide gels and electrophoresis was performed on a Model 373A automatic DNA sequencer (Applied Biosystems) for 12 to 16 hours. The sequences of oligonucleotides used as primers are shown in Table 1.

[0225] 9. DOP-PCR. As an alternate procedure we used partially degenerate oligonucleotides in combination with vector-specific (SP6 or T7) primers to amplify insert ends of BAC clones, following a previously published protocol for P1 clones (Liu et al., 1995). The degenerate primers Deg2, Deg3, Deg4, Deg6 (Table 1) gave the best results for selected amplification of insert termini.

[0226] Table 1: Primers used for PCRs and sequencing

[0227] Vector specific Primers for DOP PCR- first amplification step:

[0228] SP6-BAC1: AGT TAG CTC ACT CAT TAG GCA (SEQ ID NO. 734)

[0229] T7-BAC1: GGA TGT GCT GCA AGG CGA TTA (SEQ ID NO. 735)

[0230] Vector specific Primers (direct sequencing, nested primer for second PCR step)

[0231] SP6 Mid: AAA CAG CTA TGA CCA TGA TTA CGC CAA (SEQ ID NO. 736)

[0232] T7-Belo2: TCC TCT AGA GTC GAC CTG CAG GCA (SEQ ID NO. 737)

[0233] Degenerate Primers:

[0234] Deg2: TCT AGA NNN NNN TCC GGC (SEQ ID NO. 738)

[0235] Deg3: TCT AGA NNN NNN GGG CCC (SEQ ID NO. 739)

[0236] Deg4: CGT TTA AAN NNN NWA GGC CG (SEQ ID NO. 740)

[0237] Deg6: GGT ACT AGT NNN NNW TCC GGC (SEQ ID NO. 741)

[0238] Primers used for the amplification of *M. bovis* DNA in polymorphic chromosomal region of Rv58:

[0239] Primer 1: ACG ACC TCA TAT TCC GAA TCC C (SEQ ID NO. 742)

[0240] Primer 2: GCA TCT GTT GAG TAC GCA CTT CC (SEQ ID NO. 743)

[0241] 10. Screening by pooled PCR. To identify particular clones in the library which could not be detected by random end-sequencing of the 400 BAC clones, PCR-screening of DNA pools was performed. Primers were designed for regions of the chromosome where no BAC coverage was apparent using cosmid-or H37Rv whole genome shotgun sequences. Primers were designed to amplify approximately 400-500 bp. Ninety-six-well plates containing 200 µl 2YT/12.5 µg/ml CM per well were inoculated with 5 µl of -80°C glycerol stock cultures each from the master plates and incubated overnight. The 96 clones of each plate were pooled by taking 20 µl of culture from each well and this procedure was repeated for 31 plates. Pooled cultures were centrifuged, the pellets were resuspended in sterile water, boiled for 5 minutes, centrifuged and the supernatants kept for PCRs. As an initial screening step, the 31 pools of a total of 2976 BACs, representing about two thirds of the library were tested for the presence of a specific clone using appropriate PCR primers. PCR was performed using 10 µl of supernatant, 5 µl of assay buffer (100 mM b-mercaptoethanol, 600 mM Tris HCl (pH 8.8), 20 mM MgCl₂, 170 mM (NH₄)₂SO₄), 5 µl of Dimethylsulfoxide (DMSO), 5 µl of dNTPs (20 mM), 5 µl of water, 10 µl primer (2 µM), 10 µl inverse primer (2 µM) and 0.2 units of *Taq* DNA polymerase (Boehringer). 32 cycles of PCR (95°C for 30 s, 55°C for 1 min 30 s, 72°C for 2 min) were performed after an initial denaturation at 95°C for 1 min. An extension step at 72°C for 5 min finished the PCR. If a pool of 96 clones yielded an appropriate PCR product (Fig. 1A), subpools were made to identify the specific clone. Subpools representative for lane A of a 96 well plate were made by

pooling clones 1 to 12 from lane A into a separate tube. Subpools for lanes B to H were made in the same way. In addition, subpools of each of the 12 rows (containing 8 clones each) were made, so that for one 96 well plate, 20 subpools were obtained. PCR with these 20 subpools identified the specific clone (Fig. 1B, lower gel portion). If more than one specific clone was present among the 96 clones of one plate (Fig. 1B, upper gel portion), additional PCR reactions had to be performed with the possible candidates (data not shown).

[0242] 11. Genomic comparisons. DNA from the BAC clone Rv58 was digested with the restriction endonucleases *Eco*R1 and *Pvu*II, and resolved by agarose gel electrophoresis at low voltage overnight (1.5 V/cm). DNA was transferred via the method of Southern to nitrocellulose membranes (Hybond C extra, Amersham) following standard protocols (Sambrook et al., 1989), then fixed to the membranes at 80°C for 2 hours. The blot was hybridized with ³²P labelled total genomic DNA from *M. tuberculosis* H37Rv, *M. bovis* type strain (ATCC 19210) or *M. bovis* BCG Pasteur. Hybridization was performed at 37°C overnight in 50% formamide hybridization buffer as previously described (Philipp et al., 1996b). Results were interpreted from the autoradiograms.

[0243] 12. Computer analysis. Sequence data from the automated sequencer ABI373A were transferred as binary data to a Digital Alpha 200 station or Sun SparcII station and analysed using TED, a sequence analysis program from the Staden software package (Dear et al., 1991). Proof-read sequences were compared using the BLAST programs (Altschul et al., 1990) to the *M. tuberculosis* H37Rv sequence databases of the Sanger Centre, containing the collected cosmid sequences (TB.dbs) and whole-genome shotgun reads (TB_shotgun_all.dbs) (<http://www.sanger.ac.uk/>). In addition, local databases containing 1520 cosmid end-sequences and the accumulating BAC end-sequences were used to determine the exact location of end-sequenced BACs on the physical and genetic map. MycDB (Bergh et al., 1994) and public databases (EMBL, Genbank) were also used to compare new sequences, but to a lesser extent. The organization of the open reading frames (ORFs) in the polymorphic region of clone Rv58 was determined using the DIANA software established at the Sanger Centre.

EXAMPLES

[0244] Example 1 : Construction of a pBeloBAC11 library of *M. tuberculosis* H37Rv.

[0245] Partial *Hind*III fragments of H37Rv DNA in the size range of 25 to 180 kb were ligated into pBeloBAC11 and electroporated into strain *E. coli* DH10B. While cloning of fractions I (25 to 75 kb) and II (75 to 120 kb) gave approximately 4×10^4 transformants (white colonies), cloning of fraction III (120 to 180 kb) repeatedly resulted in empty clones. Parallel cloning experiments using partial *Hind*III digests of human DNA resulted in stable inserts for all three fractions (data not shown), suggesting that the maximum size of large inserts in BAC clones is strongly dependent on the source of the DNA. Analysis of the clones for the presence of inserts revealed that 70% of the clones had an insert of the appropriate size while the remaining 30% of white colonies represented empty or *lacZ'*-mutated clones. Size determination of randomly selected, *Dra*Icleaved BACs via PFGE showed that the insert sizes ranged for the majority of the clones between 40 kb and 100 kb with an average size of 70 kb. Clones with inserts of appropriate size were designated with "Rv" numbers, recultured and stored at -80°C for further use.

[0246] Example 2 : Direct DNA sequence analysis of BACs.

[0247] To characterize the BAC clones, they were systematically subjected to insert termini sequencing. Two approaches, direct sequencing of BAC DNA and PCR with degenerate oligonucleotide primers (DOP), adapted to the high G+C content of mycobacterial DNA, were used. In a first screening phase, 50 BAC clones designated Rv1 to Rv50 were analysed using both methods in parallel. Except for two clones, where the sequences diverged significantly, the sequences obtained by the two methods only differed in length. Sequences obtained directly were on average about 350 bp long and for 95% of the clones both the SP6 and T7 end-sequences were obtained at the first attempt. Sequences obtained by DOP-PCR were mostly shorter than 300 bp. For 40% of the BACs we obtained only very short amplicons of 50 to 100 base pairs from one end. In two cases the sequence obtained with the DOP-PCR differed from the sequences obtained by direct sequencing, and in these cases *E. coli* or vector sequences were amplified (data not shown). Taking the advantages and disadvantages of both methods into account, we decided to use direct termini sequencing for the systematic determination of the SP6 and T7 end-sequences.

[0248] Example 3 : Representativity of the library.

[0249] After having determined the end-sequences of 400 BACs a certain redundancy was seen. The majority of clones were represented at least 3 to 4 times. Maximum redundancy was seen in the vicinity of the unique *rrn* operon, as 2.5% of the

clones carried identical fragments that bridge the cosmids Y50 and Y130 (Fig. 3, approximate position at 1440 kb). The majority of clones with identical inserts appeared as two variants, corresponding to both possible orientations of the *Hind*III fragment in pBeloBACII. This suggests that the redundancy was not the result of amplification during library construction, but due to the limited number of possible combinations of partial *Hind*III fragments in the given size-range of 25 to 120 kb. To detect rare BAC clones, a pooled PCR protocol was used. Primers were designed on the basis of the existing cosmid sequences and used to screen 31 pools of 96 BAC clones. When positive PCR products of the correct size were obtained, smaller subpools (of 8 or 12 clones each) of the corresponding pool were subsequently used to identify the corresponding clone (Figs. 1A and 1B). With this approach 20 additional BACs (Rv401-Rv420) were found for the regions where no BACs were found with the initial systematic sequencing approach. The end-sequences of these BACs (Rv401-420) were determined by direct sequencing, which confirmed the predicted location of the clones on the chromosome. A 97% coverage of the genome of H37Rv with BAC clones was obtained. Only one region of ~ 150 kb was apparently not represented in the BAC library as screening of all pools with several sets of specific primers did not reveal the corresponding clone. This was probably due to the fact that *Hind*III fragments of mycobacterial DNA larger than 110 kb are very difficult to establish in *E. coli* and that a *Hind*III fragment of ~ 120 kb is present in this region of the chromosome (data not shown).

[0250] Example 4: Establishing a BAC map.

[0251] Using all end-sequence and shotgun-sequence data from the H37Rv genome sequencing project, most of the BAC clones could then be localized by sequence comparison on the integrated map of the chromosome of *M. tuberculosis* strain H37Rv (Philipp et al., 1996b) and an ordered physical map of the BAC-clones was established. PCR with primers from the termini sequences of selected BACs were used for chromosomal walking and confirmation of overlapping BACs (data not shown). The correct order of BACs on the map was also confirmed more recently, using 40,000 whole genome shotgun reads established at the Sanger Centre. In addition, pulsed-field gel electrophoresis of *Dra*I digests of selected BACs was performed (Fig. 2) in order to see if the approximate fragment size and the presence or absence of *Dra*I cleavage sites in the insert were consistent with the location of the BACs on the physical map (Fig. 3). Comparison of the sequence-based BAC-map with the physical and genetic map, established by PFGE and hybridization experiments (Philipp et al., 1996b), showed that

the two maps were in good agreement. The positions of 8 genetic markers previously shown on the physical and genetic map were directly confirmed by BAC-end-sequence data (Table 2, Fig. 3). The position of 43 from 47 Y-clones (91%) shown on the physical and genetic map, which were later shotgun sequenced, was confirmed by the BAC end-sequences and shotgun sequence data. Four clones (Y63, Y180, Y251, and Y253) were located to different positions than previously thought and this was found to be due to book keeping errors or to chimeric inserts. Their present approximate location relative to the *oriC* is shown in Figure 3: Y63 at 380 kb, Y63A at 2300 kb, Y180 at 2160 kb, Y251 at 100 kb, and Y253 at 2700 kb. A total of 48 BACs, covering regions of the chromosome, not represented by cosmids were then shotgun sequenced (Cole et al., 1997), and these are squared in Fig. 3. No chimeric BACs were found, which is consistent with the observations of other research groups for other BAC libraries (Cai et al., 1995; Zimmer et al., 1997). The absence of chimeric BACs was of particular importance for the correct assembly of the *M. tuberculosis* H37Rv sequence. The exact position of the BAC termini sequences on the chromosome will be available via the world wide web (<http://www.pasteur.fr/MycDB>).

[0252] Table 2 : Identities of genetic markers previously shown on the integrated and genetic map of H37Rv. (Phlipp et al., 1996b) which showed perfect sequence homology with BAC end sequences.

Locus	BAC end sequence	Description of genetic marker	Organism	GenBank Accession n°
<i>apa</i>	Rv163SP6	Secreted alanine-proline-rich antigen	<i>M. tuberculosis</i>	X80268
<i>dnaJ, dnaK</i>	Rv164T7		<i>M. leprae</i>	M95576
<i>fop-A</i>	Rv136T7	DnaJ hsp	<i>M. tuberculosis</i>	M27016
<i>polA</i>	Rv401T7	Fibronectin binding protein	<i>M. tuberculosis</i>	L11920
<i>ponA</i>	Rv273T7		<i>M. leprae</i>	S82044
<i>pstC</i>	Rv103T7	DNA polymerase I Penicillin binding protein	<i>M. tuberculosis</i>	Z48057
<i>recA</i>	Rv415SP6		<i>M. tuberculosis</i>	X58485
<i>wag9</i>	Rv35SP6	Putative phosphate transport receptor Homologous recombination 35-kDa antigen	<i>M. tuberculosis</i>	M69187

[0253] Example 5 : Repetitive end-sequences.

[0254] Repetitive sequences can seriously confound mapping and sequence assembly. In the case of the BAC end-sequences, no particular problems with repetitive sequences were observed. Although nine clones with one end in an *IS1081* (Collins et al., 1991) sequence were identified, it was possible to correctly locate their position on the map using the sequence of the second terminus. Moreover, these BACs were used to determine the exact locations of *IS1081* sequences on the map. Five copies of this insertion sequence, which harbors a *HindIII* cleavage site, were mapped on the previous physical and genetic map. In contrast, BAC end-sequence data revealed an additional copy of *IS1081* on the *M. tuberculosis* H37Rv chromosome. The additional copy was identified by six clones (Rv27, Rv118, Rv142, Rv160, Rv190, Rv371) which harbored an identical fragment linking Y50 to I364 (Fig. 3, at ~ 1380 kb). This copy of *IS1081* was not found by previous hybridization experiments probably because it is located near another copy of *IS1081*, localized on the same *DraI* fragment Z7 and *AsnI* fragment U (Fig. 3, at ~ 1140 kb). Furthermore, the position of a copy of *IS1081* previously shown in *DraI* fragment Y1 (Fig. 3, at ~1840 kb) had to be changed to the region of Y349 (Fig. 3, at ~ 3340 kb) according to the end-sequences of BAC Rv223. The positions of the four other *IS1081* copies were confirmed by the sequence data and therefore remained unchanged. In total 6 copies of *IS1081* were identified in the H37Rv genome in agreement with the findings of others (Collins et al., 1991).

[0255] In addition, a sequence of 1165 bp in length containing a *HindIII* site was found in two copies in the genome of H37Rv in different regions. The end-sequences of BAC clones Rv48 and Rv374, covering cosmid Y164, as well as Rv419 and Rv45, that cover cosmid Y92, had perfect identity with the corresponding parts of this 1165 bp sequence (Fig. 3, at ~ 3480 kb and ~ 900 kb). Analysis of the sequence did not reveal any homology with insertion sequences or other repetitive elements. However, as each of the two locations showed appropriate BAC coverage, chimerism of the sequenced cosmids Y164 and Y92 can be ruled out as the probable cause.

[0256] Example 6 : Using BAC clones in comparative genomics.

[0257] The minimal overlapping set of BAC clones represents a powerful tool for comparative genomics. For example, with each BAC clone containing on average an insert of 70 kb, it should be possible to cover a 1Mb section of the chromosome with 15 BAC clones. Restriction digests of overlapping clones can then be blotted to membranes, and probed with radiolabelled total genomic DNA from, for example, *M. bovis* BCG Pasteur. Restriction fragments that fail to hybridize with the *M. bovis* BCG Pasteur DNA

must be absent from its genome, hence identifying polymorphic regions between *M. bovis* BCG Pasteur and *M. tuberculosis* H37Rv. The results of such an analysis with clone Rv58 (Fig. 3, at ~ 1680 kb) are shown here. This clone covers a previously described polymorphic genomic region between *M. tuberculosis* and *M. bovis* BCG strains (Philipp et al., 1996a). *Eco*RI and *Pvu*II digests from clone Rv58, fixed on nitrocellulose membranes, were hybridized with ³²P-labelled total genomic DNA from *M. tuberculosis* H37Rv, *M. bovis* (ATCC 19120), and *M. bovis* BCG Pasteur. Figures 4A and 4B present the results of this analysis, where it is clear that several restriction fragments from clone Rv58 failed to hybridize with genomic DNA from either *M. bovis* or *M. bovis* BCG Pasteur. On the basis of the various missing restriction fragments, a restriction map of the polymorphic region was established and compared to the H37Rv sequence data. The localization of the polymorphism could therefore be estimated, and appropriate oligonucleotide primers (Table 1) were selected for the amplification and sequencing of the corresponding region in *M. bovis*. The alignment of *M. bovis* and *M. tuberculosis* H37Rv sequences showed that 12,732 bp were absent from the chromosomal region of the *M. bovis* type strain and *M. bovis* BCG Pasteur strain. The G+C content of the polymorphic region is 62.3 mol%, which is the same as the average genome G+C content of the *M. tuberculosis* genome, hence indicating that this region is not a prophage or other such insertion. Subsequent PCR studies revealed that this segment was also absent from the Danish, Russian, and Glaxo substrains of *M. bovis* BCG, suggesting that this polymorphism can be used to distinguish *M. bovis* from *M. tuberculosis*. Analysis of this sequence showed that 11 putative open reading frames (ORFs) are present in *M. tuberculosis*, corresponding to ORFs MTCY277.28 to MTCY277.38 / accession number Z79701 -EMBL Nucleotide Sequence Data Library (Fig. 5). FASTA searches against the protein and nucleic acid databases revealed that the genes of this region may be involved in polysaccharide biosynthesis. Among these putative genes, the highest score was seen with ORF 6 (MTCY277.33), whose putative product shows a 51.9% identity with GDP-D-Mannose dehydratase from *Pseudomonas aeruginosa* (accession number U18320 - EMBL Nucleotide Sequence Data Library) in a 320 amino acid overlap. The novel *M. bovis* sequence of the polymorphic region was deposited under accession number AJ003103 in the EMBL Nucleotide Sequence Data Library.

[0258] As it appears from the teachings of the specification, the invention is not limited in scope to one or several of the above detailed embodiments; the present invention also embraces all the alternatives that can be performed by one skilled in the same technical field, without deviating from the subject or from the scope of the instant invention.

Clone Rv7

:::Rv7SP6.seq:::

ATACTCAAGCTTATCTAGGCGCCAGCTTGATTGGTCTGGTTGCATTGGCCAGCTGCGCGAGCCTGGCTCACTTCAACT
ACAACAACCGCAAACAATTGCCGCTTCGGATCCGAGTTTCGGTTGGGTACGCGGCAATGGANACCATTTCTCGGTGA
ATCAGACTATTCTGAGTACTTGATCATCCACTCTGCACACGACCTGCGAACCCCGCGCGCCTTGCCGACCTGGAGC
AGCTGGCGCAACGTGTGAGCCANATCCCAGGCGTTGCCATGGTTTCGGGTGTGACCCGGCCAAACGGGGAAACCTTG
AACAGGCCCCGGGCGACATACCAAGCCGGCCAAGTTGGCAACCGGCTGGGCGCGCGCTCGCGAATGATCGATGAGCGCA
CCGGCGACCTGAATCGGCTGGCATCGGGTGCCAACTGTTGGCCGACAATCTCGGTGACTTCGCGGTCAAGTCAGCCG
GGCCGTTGCGGGTGTCCGAGCCTTGTCAGCCCTCGCTTACTCCA (SEQ ID NO. 656)

:::Rv7T7.seq:::

CAGGCATGCAAGCTTTTGGAGCGTCGCGCGGGGCGAGCTTCGCCGGCAATTCTACTAGCGAGAAGTCTGGCCCGATACG
GATCTGACCGAAGTCGCTGCGGTGCAGCCACCTCATTGGCGATGGCGCCGACGATGGCGCCTGGACCGATCTTGTG
CCGCTTGCCGACGCGGACGCGGTAGGTGGTCAAGTCCGGTCTACGCTTGGGCCTTTGCGGACGGTCCCAGCGTGGTC
GCGGTTGCGCCGCGAAAGCGGGGTCGGGTGCGCATCAGGAATGCCTCACCGCGCGGCACTGCACGGCCAGTGGCCG
CGGCGATTGAGCCATCGGGACATCATGCTCGCTTACACTCCTCGACCAAGTCGGCGGAACAGCTCGATTCCCGGAACG
CCCACGCATGGTG (SEQ ID NO. 657)

Clone Rv80

:::Rv80SP6.seq:::

AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGTAGAAAAAGATCGGTGA
GCGCATCGATTGCTCCGCCGGGTTTGGCGCTGCGGCGGGGAGCTGCCGTGACCGTCTATTGGGTGATCAGACT
GGGCTAGTTCGGTTCGGGTGGGGTGATCGAAGATCGCGGTGGCCGGCAGCGTTACTGCGGTGACAGCTGTTAAGCGGT
TACGTATCTCCACGGCACTCAAGGAATTAATCCCGAATCGGCAAACGCCTGGCCAGCGTCNAGTCCGGCAGCGCCGT
CNCGCCCCAGCACCGCTGCGGCATGCTCACATACCACCTCGATCGCTGCGGCGANTTGCTCGTCNGCCGACCGACCGG
CCANCCGGGCGGCAAACCCNGAAGACCCAAGAAATTCATCACCACCATCGCTAGC (SEQ ID NO. 658)

:::Rv80T7.seq:::

CCTTCTTGACACCCACCTCGCCATCGACCTTGAGCACTCCGTCTAGTTGGTGAACATGTGACCGGCGATCGGGCGGG
TGAACGCGTACTGGGTGTGCGGTGTGACGTTTCTTACCACGCCGTAGCGCAGCGCCTCCTCGATCTCCGACTTAA
GCGAACCCGAGCCCGCGTGAACACGAAATCNAACGGCTTGGCGTCNGCCGGCAGTCCGAGCTTGGCCGCGCCACCT
GTTGCCCTTGCGCAAGGATGTCNCGGCGAANCTTGACGTTGCCGGGCTTGANACGCCATGCACGTTGCCGAACGTCN
CGGCCAGCANGTATTTGCCGTGCTCACCGCGCGCCANCGCCTCGATGGTCTTCTCGAAGTCTCCGGGCTGGTGTACA
GCTTCTCGTTGATCTCGTTCGCCACGCCGTCTTTCGCCGCGGACG (SEQ ID NO. 659)

Clone Rv81

:::Rv81SP6.seq:::

AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGGAAAGGAGATCCCCGGG
AACCTGGTGGCAACCCCGCCATTGGGGTTGTTGGGATTGCCGATCAGCGTGAANGAAAGCTCGTCTGGAGACAGCGGG
TCGGCCGAAGCCGCAAGATTGGCCATCACTAGTGACGANATCGTGGCGCTCTGCGAGTANCCNAAGACAGTACGTTG
TTNCCGGCGGCAATTTGCTGCCGAATCGCACTTTGAGAAATGACNGCACCTGCGCCACCGANGAATCNAAAGTGAGG
TTCTTGATCAGACACCGGGTNGAGCCCTTGGGGCGTGAAGANCGCCTGCGCNATAACACCCGGGACGCTGCCACTC
ATGTNACGCGGTTGCGGANCTCNACATATCT (SEQ ID NO. 660)

:::Rv81T7.seq:::

TCCTGGTGATCGANGGCGCGGTTCCGGCCGAAATCCGGTTCGGGTCGGGTTCGCGGTTCCAACCTTGANCGCGGTCC
GCAGCTGATTACCGTGGCAACGCGGCAACTGCGCATAATGCGCATCCGAACCTCACCCGCGCGCCCGGATCA
CCCCAACCTGATCCAACGACAACCGCCCTCCCGCATACCCCGGGCGCAGCGCGGAAACTCCGGCAACCGCGCGCCA
CCGTGGCGATCGTGTGGGCGTTGCCTGACGAACANCCCATCTTCCAGGCCACCAACCCCGCCACCGACCGCGCCCCG
TCACACCCCAACCCGTGCGGATCCAGCTCAGCCACGATCTCCACAATGCGCCCATCAATCGCATTGCGCTGAACGG
GCAACTCCGCCAATCCTCCAA (SEQ ID NO. 661)

Clone Rv82

:::Rv82SP6.seq:::

AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGATCTGGTACCCATCCGTGATA
CATTGAGGCTGTTCCCTGGGGGTCGTTACCTTCCACGAGCAAAACACGTAGCCCTTCAGAGCCAGATCCTGAGCAAG
ATGAACAGAACTGAGGTTTTGTAAACGCCACCTTTATGGGACGCAACCCCGATCACCGGTGGAAATACGTCTTCAGC
ACGTCGCAATCGCGTACCAACACATCAGCATATGATTAATTTGTTCAATTGTATAACCAACAGGTTGCTCAACCCG

TCCTCGAATTTCCATATCCGGGTGCGGTAGTCGCCCTGCTTTCTCGGCATCTCTGATAGCCTGAGAAGAAACCCCAAC
TAAATCCGCTGCTTCACCTATTCTCCAGCGCCGGGTATTTCCTCGCTTCCGGGCTGTCATATTAACTGTGCAA

(SEQ ID NO. 662)

Clone Rv83

.....Rv83SP6.seq:.....

AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTANCGCCACCTCCCGGGCG
GAACTCCACGGCGTGGATNAAGGTACCGGCCGGGATGTTGCCAATGGCAGGTGTTGCCCGGCTTGANGTCCGCGTT
AGCGCCGGATTCCACCACATCCCCTTGCGAAANTCCGTTGGGTNCNATGATGTNNCGCTTCTCCCNCTCNANATAATG
GANCAACGCNATCCGTGCGGTACGGTTCGGGTCTACTCCATGTNCGCGACCTTGGCGTTGANACCATCTTTGTCAAT
GCGGCGAAAGTCNATCATCCGGTNAGCNCGNATGANCGCCGCTTTGTGCCGGGTGTAATCCGGCCATGCGCNTT
GCGTCCACCGCAACGTGCAACGGGGGCNCAACGANTTCTCNGGGTTGAACCGGTNATCT

(SEQ ID NO. 663)

.....Rv83T7.seq:.....

TGTGTGTGGTGGTAACCCATCTGAGCAGTGTGCCAAACGGGGCAGCCAGCTCCCAATTGACGTGAGCCCGCTCACTT
GCTGGGTAAGCGTCG

(SEQ ID NO. 664)

Clone Rv84

.....Rv84SP6.seq:.....

AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATANAATACTCAAGCTTGCGGGTNATNGCCTTGGT
CAACGGCACCGTGATCGGATCNGGGTCTACCGCACACATNGACTGGAGCTTCGGCGAANTCATCGCCTATGCCTCGCG
GGGGTGACGCTGANCCNGGTGACNTGTTGCTCNGCTCNGGCACGGTGCCACCTGCACGCTCNTCNAACACCTCANGCC
ACCGGAATCATTTCCNNGGCTGGCTGCACGANAGCGANNTTGTNCNCCCTCCAAGTCTAAAGGCTGGGCGANANAAGCAN
AACGTCCCGACNAACGGCACTCCTTTTCCNTTGTCTTCTC

(SEQ ID NO. 665)

.....Rv84T7.seq:.....

GAAATCATTGATGGTTTGAGTCACCAGGCGGATCAAGCCTTCGCCGAGCCAAATTCCAATCAAGAGGCCCAAGCCCGT
ACCAATCAGCCCGGCAACGAGGGATTCCGTATTATCAGCCAAAATAACTGCTCTCGGGTTACACCCAAACAGCGCAA
TATGGCGAAAAACGGTTCGCCGTTGCACGACATTAAATGTACCGGTATTGTAGATTAAAAAGATACCCACCAACAANGC
AATCAAATGAGAGCGGTTAAATTGACCGTAAAAGCGTCCGTATCTGTTTGACNGTGTCCGCTTGGGTATCCGACGT
TTCCATACGCACACCGCCGGCAGTCTTTGTTGGATGCGTNTTGAATGGCCTCATCTTTGATGATCAAATCGATGTN
GCTCAGTCTTCCGGGCATATGGAACAACCTTGGGCCGTGGAAATATCAGCAATGATA

(SEQ ID NO. 666)

Clone Rv85

.....Rv85SP6.seq:.....

CTTTCGCCAGGCGCGCGGATGTCTCATCGCTTACGAACATCATCCGAGCTTGACGCTGTCCCGAACAGATCC
GCGCTGCCGGCCGCCGCGCCACACCGTTGCCGCCGATCTGGCCCATCCCGAGGTGACCGCGAGCTGGCTGGTCAAG
CCGTCCGAGCTTTCGGGAAGCTCGACATCGTCTCAACAACGTTGGCGGCACCATGCCCAACAGCTGCTAAGCACCT
GACCAANGACCTCGCGGACGCTTTCGCTTCAACGTGGGCACCGCCACGCGCTGACCGTCCGCGCGGTGCCGTTGA
TGCTGGAACACTCCGGCGGCGGCGAGCGTGATCAACATCAGCTCCACCATGGGCGGCTGGCGGCGCGGGTTTC

(SEQ ID NO. 667)

.....Rv85T7.seq:.....

TGTGGGCTCCGATCCGGCGCGCATGGCATCGACGGCGACGCCGATCGATGACGGCCAGGCTTACGAGCTTGAGGGTGT
GAAGTTGTGGACCACCAACGGTGTGGTAGCGGACCTGCTAGTGGTTATGGCGCGGGTACCGCGCAGTGAAGGGCNC
AGGGGGAATCANCGCCTTTGTCTCGAGGCTGATTCCGCCGGGATCACCGTGGAGCGGCGCAACAAGTTTCATGGGACT
GCGTGGCATCGAAAACGGCGTGACCGGGCTTCNTCGCGTCAGGGTGCCCAAAGACAACCTTGATCGCANGGAAGCGACG
GTCTGAAGATCGCGCTGACCACACTCAACGCCGACGGCTGTCCCTACCGCGCATCAACCGGAGT

(SEQ ID NO. 668)

Clone Rv86

.....Rv86SP6.seq:.....

GAGCTGGCCGAGCTGGACCGGTTACCGCGGAACACTACCGTTCTCGCTCGACGACTTTACGAGCGGGCTTGACGCGCG
CTGGAACGCGGCCACGGTGTGCTGGTGTGCGCGCCGACCGCGCTGGCAAGACAGTGGTGGCGAGTTCCGCGTGCAC
CTGGCGCTGGCGGCCGCGAGTAAATGTTTCTACACCACGCCGCTGAAAGCCCTGAGCAACCAAAAGCACACCGATCTC
ACAGCAGCTACGCGCGTGACAGATCTGGCTGCTGACCGGTGACCTGTCTGTCNCTCAACGGCAACCGCGGTGGTGGTGA
TGACCACCGAAATGCTGCGCAACATGCTCTAC

(SEQ ID NO. 669)

.....Rv86T7.seq:.....
GATCTCTGGATCGGCGGGGCTCTCCGGGCGGCTCGGCGACCTCAGCGGGCCGCGCCTTCCGGCCGAACCATTCCT
AGCCATAGATGACCGCACCTCGATGCACGGTTTGGCGGCAACGCGGCAAGCGTCNGTCGGGCCCAGCCGCGGCAATG
CGGGTACCCGGGAGCGCGGTCTGTANACCANCGCTGGACTGCGTCGCGCGGTGCGTCNACNTCAAAGTCCCCGGCGT
CCCATATCGCGTATGACGCGGGCGCGCCCGGCACCANGGGTGCCGATCCGGCCGTCTCGAACACCACCGGCCCCGCGCAG
CCGCGCGGGTCCGGCAGCNAACCCGCGCGCGGATACCCGCTGCCGCGTGCGTGATTGACCGCCGCGCGCACGCT
GGCCANGGATCAAAGCCCGTG (SEQ ID NO. 670)

Clone Rv87

.....Rv87SP6.seq:.....
GGACCGGTAGCCCGCCAGGCGGTGAGGTTGCCCTTCCAGTCCACGCCGCTGTGGTGGCGAACCGCTTATCTTCAAT
CGAGACGATCGCCAGCTTCATCGTGTGGCGATCTTGTCCGAGGGCACCTCGAACCGGCGTGGAGTNCAGCCACGC
GATCGTGTGGCCTTCGCGTCGACCATCGTCGATACCCGAGGCACTTGCCCTCGAGCAGCTGGGCCGAGCGGTGGC
AACGACCTCAGANGCACGATTGGACATCAGCCCTAGCCCGCTGCGAACGGGAACGTGAGCGCAGTGGCGACGACACT
GGCCAACAGACAGCACCCAGCCAGCTTCAGAACGGTGATCGCGGCGGGGAAGCGCTCGGGCATGCGTNTACAGTAGC
GACCTCCTGTCACTCCACGTGCCGCTCGGTCCAATAGAATCTTCCGCGGGCGGGTGAATCTCTGCNGGATCGGGGCGN
GGCGC (SEQ ID NO. 671)

.....Rv87T7.seq:.....
GCTCGTTGCCGGCGGCGATCTCGTCGAGCTCGTCTTCCATCGCCGCGGTGAAGTCGTAGTCGACGAGCCGACCGAAAT
GCTGCTCGAGCAGACCGTTACCGCGAACGCCACCCATGACGGCACCACTGCACTGCCCTTCTGTGCAGTNGCCGC
GATCCTGGATGGTCTTGATGATCGACGANTAGGTGACGGGCGGCGATGCCAGCTCCTCGAGCGCTTTGACGAGCG
ACGCCTCNGTGTNNCGGGCCGGCGGTTGGTGGCATGGCCGTCTGGGGTCAACTCGACNATGTCCAACCGTTGACCCG
GGGTGAGATGGGGCAGTCGCCGCTCGGCATCGTCAGCCTCGCCGC (SEQ ID NO. 672)

Clone Rv88

.....Rv88SP6.seq:.....
GTCTTTTCGATGGCTGCTTCTTCGGCGCTGACGCTGGCGATCTATCACCCCCAGCAGTTTCGTCTACGCGGGAGCGATGT
CGGGCCTGTTGGACCCCTCCAGGCGATGGGTCCCACCCTGATCGGCCTGGCGATGGGTGACGCTGGCGGCTACAAGG
CCTCCGACATGTGGGGCCCGAAGGAGGACCCGGCGTGGCAGCGCAACGACCCGCTGTTGAACGTCNGGAANCTGATCG
CCAACNACACCCNCGTCTGGGTGTACTGCGGCAACNGCAAGCCGTGGATCTGGGTGGCAACAACCTGCCGGCCAAGT
TCCTCGAGGGCTTCGTGCGGACCATCAACATCAAGTTCCAAGACGCTACAACGCCNGTGGCGGCCACAACCGCGTGT
TCGACTTCCCGG (SEQ ID NO. 673)

.....Rv88T7.seq:.....
GCCAGGTGAGGTCCCATGCGCGTGGGCCATTGATGCTGATCGCCAGGACGTCAAANATTTGGTCCGGCGTCAGCTGG
GCGAAAAACGTGGGCCCCAGGACTTGCCCGGAGCTGCCCGGTTCCCGTCGCGCAGCTCGGCGGCCCCGGTCAGAAAN
AAATTGCGCCAGGTGCGCACACTCCGCGCCGTANGCCAGCTGCTCCAGGGTGTGGCATAGAGCCCGCGGGCCGCGAGCG
TGCTCGCTGTGCGGAACACCGCATGGTTCGAGAAGCGTTGCCGCCAACGGAAATCACCTGCGTCNAANGCTTCGCGG
GCCAACTCCAGCACTCGGTGATG (SEQ ID NO. 674)

Clone Rv89

.....Rv89SP6.seq:.....
NAAACGTTCCGGCTTNGGTGCCGGGCGCTTATTTGCGTCTCTGGGATCACNCTCAGTCGCCGGGCGGCTGCCGTGGGC
TATNANTTGACCCGANCCGAAAAATCCGCACNANAACGTCNAGTAGCGGCCTGCAGAAATGCATCCTCGGCGAANCNG
ACTACCGGTGGACANCNACAAGCGCCGCGGAACAACGCACTGGCCCCGAGGGATNGGCGTCTATCGGCCCCCGCCGTCG
AACTNGGAACAGACNGTGGGTCTACCGTGATCTGGTGGGAATGCTCNACCANACCTTCCCNANNGCTACGGAACNA
CGGCGCGATATTNCGCCNTCCCANCTCGAGCCTGACNCTNGATATCGTCGANNCTCACCATCNCGATCNGCTGTGCCG
GTNTTGCTCGGACTN (SEQ ID NO. 675)

.....Rv89T7.seq:.....
CGAACGACGAACNCCNCAAGCCATGGTGGTTGGCGCGCTCAAAGGTCCGCGGTGCCCACTACTGGAAAAATCGCCTTG
AGCGTCNCTCGACCNCCGCTCGAGTTGGGTGNTAACGAAATACCTGATGCCGATCANGTCNACGTCTCCGTGCGNCC
AACGTGACGCGGCGACCACTCTACNANGTCTCGGTNCCGCCNCGGCCAGNGCACCACCACTGACNAATCCNTGCGCC
NTCGGGCCNAGCANTCCCGGTGCNACCGNGGTGGGTCCGCGGATGGTNGGGTGTNCTCNNTACNGGAACGCCAGCGCN
ATCANCATCGGCANACTCNCGTGATGTGCCGCGGGCAACCATCCCCACAATGATCNGGTGCGTCTGATCAGGCN

(SEQ ID NO. 676)

Clone Rv8

.....Rv8SP6D.seq:.....
TTAGGCGTGACGGCCACCGGGGCGCACTCCGCACAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTC
GCCGACTTTCGCGGGTACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGC (SEQ ID NO. 677)

.....Rv8T7D4.seq:.....
CGTCACCCCGATGCGCCAGATCGGGGCTTCGCAGATAAAGCACGAACTGGCGGGCAAAACGTCGATCTCGGAGCCGG
AAGGGCAATCAGCCGACCGTCGACGAACGACACCGGCGAGACCACTTAGGCAGTGACGGCCT (SEQ ID NO. 678)

Clone Rv90

.....Rv90SP6.seq:.....
CTTTTCNCGATGTCTCATGATNCCNANGGAGAACNNTGCNANCNCNGCCGCTGACNTNGCNCACCGCTNTGGCNGNGG
TGACATTGGTGGTGGTTCGCGGGCTGCNACGCCCCGACTCGANGCCGANCCATNTNTTGGCGCCGACCGCNTNTCGTCTC
NACCGCANNNCCNATCTCNGCCGCNCCCGGTGGANCTACNGCTNCTTCGCCATCTCTCGCCNATGGCTCCNGCGNNTC
GCNCAACGTNTGGTTGGTNANCTGCCTACCTGGTCNT (SEQ ID NO. 679)

.....Rv90T7.seq:.....
GCTGCGCCAGTCGTTCCGTCGCGTCATGCCGTTGGACCNACCATCGGAGTTAGTTGCCGAACCGCGGACCAACCGCAAG
CACCCGGTCCTGGTCGCGCACCGCGCTCGGCCAACCGCTTGAGCACCACACGCGCGAGCCCTCGCCGCGCACGAATCC
ATCCGCGTTGGCGTCNAANCTGTNGCATCGGTTCGCTCGGTGACAGCGCCGACCACTTGGACAGCGCGATGGCGGTGAA
CGGTNANTAGGTGACCTGCCNCCNCGCCCGCAATGCCACCTCCGCTTCAACNATGCGAATGGTCTGACACGCCNAG
TGAATTGCCACCGACGACAACAAAATCGGTATCTNCGCGACGGCGGACACGCNATCCNACTGATACTCGATCCGC
CCCACCGCTTGNANCTCCGGGTTCCNGTGCTCATGTACNTCATGTGCGTCTGCGCNCGATATTGACGATCGTGTTTC
CCACGANNANAGANCCTCATCACGCCGGTTCGAGTGCCG (SEQ ID NO. 680)

Clone Rv91

.....Rv91SP6.seq:.....
CTGTGTGCGGNCGGCGCGATATCGGCCTTTTACTAACCGAACCCGATGTGGGCTCCGATCCGGCGCGCATGGCATCT
ACNCGACGCCGATCGATGACGGCCAGGCTTACGAGCTTGAGGGTGTGAANTTGTGGACCNCCAACGGTGTGGTAGCG
GACCTGCTANTGGTTATGGCGCGGGTACCGCGCAGTGAANGGCACCGAGGGGGAATCANCGCCCTTGTCTGTCTANGCT
GATTCTCCCGGGATCACCNCTGGAGCGCNCNCNANTTTCATGGGACTGCGTGGCATCCAANACGGCGTGACCGGCTTCA
TCCNTCNGGGTGCCCAAAGACAACTTGATCNGCNGGGAAGCGACGTCTGAANATCGCGCTGATCNCACCTCAACGCCGG
ACGCTGTCTTACCGGCGATCGCACCGGANTTGCCAANCCGCGCTNANNATNCGCGNGAATGNCCGTCCACNANTGCAT
GG (SEQ ID NO. 681)

.....Rv91T7.seq:.....
TGGGGTGCCGGGCGCCGAGTTGCGTCCCTGGGATCACGCAGAGTCGCCGGCGGCTGCCGTTGGGCTATGAATTGCACC
GAGCCGGAATCCGCANCAAACTGCGAGTAGCGGCCTGCAGAAGTGCANCTCGGCGAAACGGAGTACGGTGGACA
ACGAAAGCGCCCGAACNACGCACTGGCCCGAGGATTTGGCGTCAATCGGCCCGCGCGTCAACTTGAAGANAC
ANTGCGGTTCTACCGTGATCTGGTGGGAATGCTCCAACNNACCTTCNCCGAAAGCTACGGAAGCNACGGCGCGATNTT
CGGCCTTCCAGCTCGACCTGACGCTGGAAATCG (SEQ ID NO. 682)

Clone Rv92

.....Rv92SP6.seq:.....
NGGCNNGGAAGTTAATGCCCTACTGGTTCNATGCTCNACNTCNCNGTGACNNCTGCNCCGACCGCGCGAGGTCTCT
GNCCGTNACCACCGANCNGGCGATCCGGGACTCTNGTACGCATCCAACANNGANCAACGTGCACGGGCGGAGTNGTNC
CGCCACTTCGNCNATGACGGGGTCGATCCNTTCGACGTCCGTGCGCCGCGTCGGTCGAGTGCGGGTCACNCTCCNNGTA
CTCGACCNCACNGACGAGGAGTTCGANCCATCTACGTGTGGACGAAACANATCTTCTGTCCNACGACTACACCACC
ACCCAGGCCATCGCCGNCGCCCGCGANGCCCTTCGACGCCNTACTGGTCCNNGNGGNGCGCTCTCCGGTTGTCTNNC
NCNTGNCGTGTTCCCTTCACNCACTGCCCNACATCGANCCGAGCNATNCNANGTCCGTCAATC (SEQ ID NO. 683)

.....Rv92T7.seq:.....
GGACACTGTTCCGCTGCCCCCTCGTCAAAGCCGGAGTGGTCTGTGCTGCGCCGGACCCGACCCGACCTTCAGCGGGGGTT
CACAGCTCCGTGGGTGCCGTTACTTCCGATCGCCGCGAGTGTGCGCTGCCGTGGCTGATGCTGAACCTCACCGCGTT
GACTTGGATCCGGTTCGGGATCTGGCTGGTGGCCGGAACCGCGATTATGTGCTACGGGCGCCGGCACTCGGCGCA
TGGCCTTCGGCAAGCNCNANANAACGCGACCCGGAGGTGTTGAAGTACGCTTCGCCGCGTATTTACAAATTGCNTTATA
TGTCTACACATAAGACGCAAACTGCTCTATTGTCAANTCCANCCTGGTGTGGCNCATGAAGATGTTTGG

(SEQ ID NO. 684)

Clone Rv94

.....Rv94SP6.seq.....
TCCTTCTCGGTATCGGTTTGGGCTGTCAACANAGTTGGTAGTTCTTCACGTNCTGTTGTTTCGAGCGTCNAGCCGTCG
CGCGTGTGNANGTCNCCGGACGCGTATCCCGCCAGGCCGGTCANGGTGCCCTTCCANTCCACGCCGCTGTGGTCGGCG
AACGCTNATCTTCAATCGAGACCATCGCCAGCTTCATCNTGTTGGCGATCTTGTCTNNACGGCACCTCNAACCGGCGCT
NCTAGTACNCCACNCNATCNTGTTNCCTTCNCGTACATCCTCGATNCCNCNTGCACTTTCCCTCGANCNCCTGGGC
CGAGCCGTTGGCANTNACCTCNGAGCCCCATTGGACATCANCCANCCCGCTGCGAACGGGAACGTCAGCNCNCTGG
CGAACCTGGCCAACAN (SEQ ID NO. 685)

.....Rv94T7.seq.....
CACNCCGTGATCGCNAGCCCCNGTAGAAATNGTTAGCCAGTTGGTGCGGCGCTCGTTGCCGGCGGTNATCTCGTCGA
GCTCNTCTTCCATCGCCGCGGTGAAGTCGTACTCGACNAGCCGACCNAATGCTGCTCNAGCAGACCGGTTACNNNA
ACNCCNCTCNTGACNGCACCAGTGCNCTGCCCTTCTTGTGACGTACCCGCNATCCTGGATGGTCTTGATGATCNAC
TANTNTGTCGACGGGCGGCGGATGCCATCTCCTCNAGCGCTTTGACCAGCGACNCTCGGTGTATCGGGCGGCGGG
TTNGTGCGATGGCCGTCTGGGGTCANCTCNACNATNTTCANCCGTTGACCCGGGGTCACA (SEQ ID NO. 686)

Clone Rv95

.....Rv95SP6.seq.....
TGGCCTTCTTGNCANGGGCANNACATNNGCTATNGCGAGCGTGTAACCGATCATCNTCCNGGCGACTGTGGCCTGANCG
GCAAGGGTNGCCTNATTCNTCCTCGNGGCATGGTTNCCACACGGAATGNCGGTAAGTCTGGTCGGCAACCTGGCCC
GCTGCCGGTTGGGTTTCGGATTCGCTCGGCTANTAAAGTGCTCGCCTGGTGTNACNACTAATCNCNATATACTTANC
GGGAGTNGNCGTCCGATCCTNGCCCTGCCGCGGGGATCNCGTTCCGANACCCGCCACCGGAACCTCNAANGTGGCG
TCATCGGGCTCTACGCGCCATCTTCCCGGATTCTTCGCGGCGNGGTNCCGNGGGACCCCGGACTGTGACNGGCCCAA
CGGCTCATCATCG (SEQ ID NO. 687)

.....Rv95T7.seq.....
CCGGATAGCGGTGTCTGAACCTTCGCCCCTCCCTCCANCGCATTGAGCTTCAGCCCGACCGGCAGGTNNGGAGTCGGC
ATCGGGTCTTCGCCCCGACCCCGCTGGCTAAATANCCACCCCGAGCGCGGTACGGTCTTTGCACCGGGACGACGC
ATACCGGCAGCGCGAATCNCNCCGCGGGTGCAGCNTGAACGTCCAATACCANTCNAACAGTGTCCGCGCGTNAAC
CCGANCCGGCGGTTCGCTTCNGTAATCAACGGCTCCTGCGCAACCACTGCAAGTCCCGGTGCCACCGGCGTTGACGA
TCTTGATGTCTGCGANCTCGCGCACCAGCTCGACGGCCCGGGCA (SEQ ID NO. 688)

Clone Rv96

.....Rv96SP6.seq.....
CCTCCCGACCACATACAGGCAAAGTAATGGCATTACCGCGAGCCATTACTCCTACGCGCGCAATTAACGAATCCACCA
TCGGGGCAGCTGGTGTGATAACGAAGTATCTTCAACCGGTTGAGTATTGAGCGTATGTTTGAATAACAGGCGCAC
GCTTCATTATCTAATCTCCAGCGTGGTTAATCAGACGATCGAAAATTTATTGACAGACAGGTTCCCAAATAGAAAG
AGCATTTCTCCAGGACCAAGTTGAAGAGCGTTGATCAATGGCCTGTTCAAAAACAGTTCTCATCCGGATCTGACCTTT
ACCAACTTCATCCGTTTCACGTACAACATTTTTTAGAACCATGCTTCCCGAGGCATCCCGAATTTGCTCCTCCATCCA
CGGGGACTGAGAGCCATTACTATTGCTGTATTTGGTAAGCAAATACGT (SEQ ID NO. 689)

Clone Rv9

.....Rv9SP6.seq.....
CTTCACNTCCGTACGGCTCGGGTACGCTTCGGTCNCATTGTGCGAGTGATAGATGACGACCGGGACCTCGTCGGCATC
TTCCATAGCCCGCCACACCTTCAGTTGCTCACCGGAATCCAACCGGTANAAGGTCGGCGANCGCTCNGCATTGGTCAT
CGGGATATGCCGCTCGGGACGGTCANAGCCCTCGGGTCCGGCCAGCACTCCGCAGGCTTCGTGGGGTGGTCGCGACG
CGCATGGGCCACCATCGCATTACCCAGGTCTGCGCGAATCACCAGCACGTANACGGTTCCCTTTCTAAGCAACACCGA
ANTTTTCAGGACCCGAATGCTCCGGGAAACATGTCACGGTAGGTGCGGTATTCCGGCTACCGGCTGANCATTGAGCACGC
CGGCCAGCACCGCAGAACAGGCAATCAGCCGCCGCCGACCCGACCGCGG (SEQ ID NO. 690)

.....Rv9T7.seq.....
CAGGCATGCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCAGCCACCACGCGCGGGTCGGGCGCCGGGCC
CGGGCCGCGAGGCTGCTCCGCTCGGTGATGGCAGCCACCGCGACACCACCGGCTGCGCTACGTCGAGCCATACCGG
GCGGAGCTACATCGGCTCGGCCGCCAGTGTTGGGGCCCTCTTTCGAGGTCGAGGTCGATACCGATTGCGCATCCGC
AGCCGCACCTTGACGACAGAACCGTGCCCTACGAATTGCTTGTCGGGCGGGGCCAAAGAACAGATTGGCATCCTGGC
GCGATTGGCCGCGCGGCGCTGGTCGCCAAGGAAGACCGGTTCCGGTGCTGAT (SEQ ID NO. 691)

RvXXXT7 corresponds to the T7 end-sequence of the clone RvXXX.

RvXXXIS 1081 corresponds to a region located close to a copy of the IS1081 repetitive sequence (Insertion element).

The character « - » denotes an uncertain base residue.

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:::X0001SP6.seq:::

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TCGGGTTTCCACACGCGCGGTTTGACCCTAGTCATATGTAATCATGTGTACCATGTGCGGGCGCTTTTCGACGGCCG
CGAACCACCGGA-ATTTCTGTGATTTCACCTGCATGCGTACCATCTGGACAATTGAGCA-TTGTCT-
TCGCGGTGGTTCGG-CGGGTTGCGTGCCGCGCTGCTGCGA-ATGCACCA-
TAAGCCCGAACCACCGGCTTGGTGACCACCGCAGCTGCGTGTGGGGGTAACCACTCCGCGACCCCAAGGATGGT
CATTTCCAATGAACCGGCTGGACTTCGTCCA-A (250 bp, 282)

(SEQ ID NO. 692)

.....X0001T7.seq.....

GTCGCGGTTTCGATCGACCCGATCTTCACCTCGTAACCTCGATGCTTAGCAGGATCCAGCTTGACCGCGTTTTGGCTCT
 ACCCATCTCTTTGAGTGGCGCCGTCGCTGTGCCCATCGGTGTTTCATGACGAACGCTTCGAAAGACTTCCTCTTG
 AGCCGGAATGTCTGCGTAAGTAAGTTCATGTCTCGGGAAGTAGACCCGGTTCGCTCCAGCTGGTACTCTTCGAGG
 TCCGCTTCTCGCCGGATCCGATAAACACGGCCCCAGGCCAGCGGTGAGTTGCAACGGCTTCAGGTAGGTGTTT
 ATGCGGCGGACTCCGGGAGTGCAGAGAAATAGCGGTTCGCGCGTAGCTGTAGACCGGATGGTTTCCGCCCAGGCTGACG
 TCGAAGATGCCTCCTTGGAAGGGGCGCGA (SEQ ID NO. 693)

(SEQ ID NO. 693)

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.....X0002SP6.seq.....

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AACTCAAGTTTTTACGGTGATCGCGCATCACCTGGTTCATGAAGTGAAGCAGCGCAGCGCTTCTTTTTCGGCCGCA
ACATGAGCCAGCCTCTCGTCGGCGGTGCGGTGCAGGTGCTCGGGCAGCTCGGCCGCGCAGCCGCCTGACCCTGAAA
CCAGCTTCATATCCCGCGAC-
AACGACGCCAGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCTTCTCCACCGACCAGGGCCCGGG
TGT (SEQ ID NO. 694)

(SEQ ID NO. 694)

.....X0002T7.seq.....

GTGCAGGTTTTCGACAATGTGGTGCCGGTTTCGGCGGCTACGTGCCATCGAGACACTGGCGCA-GCTATCGCACCCGTT
ATCGGTCGCGAGCAAATCGCGGTATGCGTTCTTGAGCATGAGTCGGCGACCGTCGTCATGGTCGACACCCACGACGG
AAAGACGCAGATCGCCGTC AAGCATGTGTGCCCGGATTATCAGGACTGACCTCCTGGCTGACCGGCATGTTTGGTC
CGGATGCCTGGCGCCCGCGCGCTGGTCGTGGTCGGTCGGATAGCGAGGTCAGCGAATTCTCGTGGCAGCTCGAA
AGGGTCTCGCCGGTGCCGGT

(SEQ ID NO. 695)

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:::X0003SP6.seq:::

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TTTGAGTCATGCGCCCGCCTCGACCACGAA-ATGCACGTCG-

GGTTCGATCGACCCGATCTTCACCTCGTAACCTCGATGCTTAGCAGGATCCAGCTTGACCGCGCTTTGGCTCTACCCA
CTCTTTGAGTGGCGCCGTGCGCTGTGCCCCATCGGTGTTTCATGACGAACGCTTCGAAAGACTTCCTCTTGAGCCG
GAATGTCTGCGTAAAGAAGTTCATGTCCGGGAAGTAGACCCGGTCGCCCTCCACGTGGTACTCCTTCGAGGTCCGC
TTCTC (SEQ ID NO. 696)

(SEQ ID NO. 696)

.....:X0003T7.seq:.....
GTCATGTGTACCATTTGCGGGCGCTTTTCGACGGCCGCGAAACACCGGAGATTTCTGTGATTTCACTGCATGCGTA
CCGTCTGGCACAATTGAGCAGTTGTCTGTGCGGGTGGTTCGGCCGGGTTGCGTGCCGCCTGCTGCGAGATGCACCAAT
AAGCCCCAACCACCGGCTTGGTGACCACCGCACGCTGCGTGTGGGGGTAACCACGCCGCGACCCCAAGGATGGTC
ATTTCCAATGAACCGGCTGGACTTC-TCAACAA (SEQ ID NO. 697)

Clone X0004
.....:X0004T7.seq:.....
AACAGCGCGGTTGAACTGATAGGTGCGGCCCGGCTCGAGCAGGCCGGGCCATTTGTTTCGATGCGGTTACCGAAAGAT
CTCTTCGGTGACCTGCCCGCCCGGCCAGCTCGGCCAGTGCCCGGCGTTGGCCGCCGCGGCCGACGATCTTGGCGT
CCACGGTGGTTCGGGG (SEQ ID NO. 698)

Clone X0006
.....:X0006T7.seq:.....
GCATCTGGGCTGGCGGTGGTTCGCCGCTCCGAAGCCGTGCAACACCATCGCCAGCGGGCTTCCACATCAACGACCA
TTTCGGCCAGCTTGC GGCGCATCAGCGGCTTGTGATGAGCGCCCCACCGAATGCCCGCCGCTGCCCGGCGTA-
CACAGCGATTTCGACCAGCGCGCGCGCGCTTGCCGAGGGCGAACGAAGCGGTGCCCAACCGCAATCTGTTGGTCAG
CTCCATCATGCGGGTGAGTCCCTTGCCG (SEQ ID NO. 699)

Clone X0007
.....:X0007SP6.seq:.....
ATCGGTTTCCAGCAACAGCCGATCGACGGCTTCGCCCA-
GGCCGCTCCCGGGCGACCCGACCATTTGCTGTGCGCCGCGTAACGCCATCACGGATGACGCGCAGTTCTGTCGCTGTCTA
GCTCCACCATCGCCTGCACACCGGGCGGCCAG-ACCCATTGGCCGTCGCACTCGTA-
AGCAGGTAATCCTCGTCGACGGACTCGGTAACCACCGCCCGCAGCTCCGCTGCCAGGTGCGCGGGGTTGACACCGGC
GGGCATCGGGATGGACGACGACGCGGTGCTGACGGCGCCTGTC (SEQ ID NO. 700)

.....:X0007T7.seq:.....
AGCGGTTTCCCA-
GCGGGATGTGCTGTGAGCGCCGCACCACCAGCGCCGACGCTAAGGATGGAACGCACGGCATCTTCTGACGCGTAACC
GCGTTGTGATCGCGAGCTGAGGAGACGGTATGGGGGAGGGTTCTCGGAGGCCATCTGGGATGTTGATGTCTGTCGAT
CTTGAGCCGGTGCAACTCGTCGGCCCGGACGGTACGCCGACGGCCGAACGCCGCTACCACCGTGACCTTCCTGAGGA
AACGCTGCGTTGGCTCTACGAGATGATGGTGGTCACCCGCGAGCTGGATACCGAATTCGTCAATCTGCACG
(SEQ ID NO. 701)

Clone X0008
.....:X0008SP6.seq:.....
CAAGCTTCCACAGGTAGGGATCGAGGAACAGCGGTTGAACTGATAGGTGCGGCCCGGCTCGAGCAGGCCGGCCATT
TGTTTCGATGCGGTTACCGAAAATCTCTTCGGTGACCTGCCCGCCGCGGCCAGCTCGGCCAGTGCCCGGCGGTTGGC
CGCCGCGGCAACGATCTTGGCGTCCACGGTGGTTCGGGGTCATGCCCGCGAGCAGGATCGGCGAGCGGCCGGTCAGCC
GGGTGAACTTCGTGAAAGCTTGACCCTGCCGTGCGGGAGGCGAACCACGGTCGGTGCGTANCTCCACCAAGCCCGG
GCAACCTCGGGGGTGGCGCC (SEQ ID NO. 702)

.....:X0008T7.seq:.....
TGGACCTCATGACAACGCGGGCGGCGATTACCCCCGTACCGCCAGCAGCATGACGGCGGTAGCGAACACCGCCGGAT
GCAGCGCAGGTGCGTCGATGTGCTCACGGAATCGCCCCGCCACCGCGATCTCGAGGATCACCAGTGCCACCCCTGC
AGCGCGACACCGACGATTCCTGTACCCGCCACGCCGATCAGGCCCTGGGCCAGCTGGCGTATATGGCGGCGATGGTG
ACGATGGCCAGCGCCACATACATTGTGGCGGCCAGAACCACGGCGTTGGGGCGGCGGTGATGAACACTAGGCGACG
CAGATCGCCCGGGGTCAACAGGTTGACCATCAGAAAGCCTGCGA (SEQ ID NO. 703)

Clone X0009
.....:X0009SP6.seq:.....
TTTGGTGCGGCCGGCAATCAACTTC-GCTC-
CAGCGGTTTCCAGGCGGGATGTGCTGTGAGCGCCGCACCACCAGCGCCGACGCTAAGGATGGAACGCACGGCATCT
TCTGACGCGTAACCGGTTGTGATCGCGAGCTGAGGAGACGGTATGGGGGAGGGTTCTCGGAGGCCATCTGGGATGT
TGATGTCTGTGATCTTGAGCCGGTGCAACTCGTCGGCCCGGACGGTACGCCGACGGCCGAACGCGCTACCACCGT
GACCTTCCTGAGGAACGCTGCGTTGGCTCTACGATATGATGGTGGTCACCCG (SEQ ID NO. 704)

.....X0009T7.seq:.....
CGCCCAGGGCCGCTCCCGGGCGACCCGACCATTGCTGTCGCCGCGTAACGCCATCACGGATGACGCGCAGTTTCGTCTG
CTGCTAGCTCCACCATCGCCTGCACACCGGCGGCCAGGACCCATTGGCCGTCGCACTCGTAGAGCAGGTAATCCTC
GTCGACGGACTCGGTAACCACCGCCGCGCAGCTCCGCTGCCAGGTCGGCGGGGTTGACACCGGCGGGCATCGGGATGG
ACGACGACGCGGTGCTGACGGCGCTGTCGCGACGCTGAGCTCGGACACAGCTAGTAAATGTAGCCTAACCTACTTA
ATGGGTCGACAGCCCCCGGGGTCGTGCGATGTCCAACGTTGCTCGACTGGAAGAAAATGCTCGTCGGGGAGCAAATG
GCACC (SEQ ID NO. 705)

Clone X0010

.....X0010SP6.seq:.....
AATACTCAATCTTGATCGGTTTCCAGCAACAGCCGATCGACGGCTTCGCCAGGGCCGCTCCCGGGCGACCCGACCA
TTGCTGTCGCCGCGTAACGCCATCACGGATGACGCGCAGTTTCGTGCTGTCTAGCTCCACCATCGCCTGCACACCGG
CGGCCAGGACCCATTGGCCGTCGCACTCGTAGAGCAGGTAATCCTCGTCGACGGACTCGGTAACCACCGCCGCGCAGC
TCCGCTGCCAGGTGCGCGGGGTTGACACCGGCGGGCATCGGGATGGACGACGACGCGGTGCTGACGGCGCCTGTGCG
GACTCTGAGCTCGG (SEQ ID NO. 706)

.....X0010T7.seq:.....
GGATGTGCTGTGAGCGCCGACCAACAGCGCCGACGCTAAGGATGGAACGCACGGCATCTTCTGACGCGTAACCGCG
TTGTGATCGCGAGCTGAGGAGACGGTATGGGGGAGGGTTCTCGGAGGCCATCTGGGATGTTGATGTCTGTCGATCTT
GAGCCGGTGCAACTCGTCGGCCCGGACGGTACGCCGACGGCCGAACGCCGCTACCACCGTGACCTTCTGAGGAAAC
GCTGCGTTGGCTCTACGAGATGATGGTGGTCACCCGCGAGCTGGATACCGAATTTCGTCAATCTGCAGCGCCAGGGGG
AAGCTGGCGTTGTACACGCCCTGTGCGGGCAGGAAGCCGCGCAGGTGGGTGCGGGGCTTGCTACGAAAACCGA
CTGGTTGTTCCC (SEQ ID NO. 707)

Clone X0012

.....X0012SP6.seq:.....
ATCACGACAACAGCGACGGTGTGTCGGATCAGCGGCCCCCGTTGCCGGGCAATGTTGAGGCGTTTCTGCGTCTGGTT
GAGGCCGGCTGGGAC-
CCGAGGTGGCTCGTCGGCCACATGGGCAGCACACCACCGTGGTGATGCATCTAGACGTGCAGGACCGTGCCGCTGGC
CTGCA (SEQ ID NO. 708)

.....X0012T7.seq:.....
GCGGCTACGTGCCATCGAGACACTGGCGCAGGCTATCGCACCCGTTATCGGCTGCGAGCAAATCGCGGTATGCGTTT
TTGAGCATGAGTCGGCGACCGTCTGTCATGGTCGACACCCACGACGGAAGACGCGAGATCGCCGTCAAGCATGTGTGC
CGCGGATTATCAGGACTGACCTCCTGGCTGACCGGCATGTTTGGTCGCGATGCCTG: (SEQ ID NO. 709)

Clone X00013

.....X0013T7.seq:.....
TACAAGCGGCACCTCGCCGGTGAACGTGACCGTTTCGCACGCTGCGCACCGCCGCGGGCGCGTGCTCGGCGCGCCGGC
GGCCCCCGAGGCTGAGAGGGGAACCAACCATGCAGGTGAACATGACGGTAAACGGCGAGCCCGTCACCGCCGAGGT
CGAACCCCGGATGCTGCTGGTCCATTTTCTCCGTGATCAGCTGCGGCTCACCGGAACTCACTGGGGCTGTGATACCA
GCAACTGCGGGACATGCGTGGTGGAGGTGACGCGCGTGCCGGTGAATCCTGCACGATGCTCGCCGTGATGGCCTCC
GGGC (SEQ ID NO. 710)

Clone X0014

.....X0014T7.seq:.....
AGCGGCTGGTTACGACTCCCTGTTGTGATGGACACTTCTACCAACTGCCCATGTTGGGGACGCCCG-CC-
TCCGATGCTGGAAGCCTACACTGCCCTTGGTGCGCTGGCC-C-GCGACCGAGCGGCTGCAACTGGGCGC-
TTGGTGACC-GCAATACCTACCGCACCC-ACCCTGCTGG-CAAA-
ATCATACCACGCTCGACTTGGTTAGCGCCGGTCA-CGATCCTCGGCATTGGAACCGGTTGGTTT-
(SEQ ID NO. 711)

Clone X0015

.....X0015SP6.seq:.....
ACGCGCGCGATCATATCTGCTATGGATGTACAATTCAGCTCTTGCTGTTATACCAGTATATGGTGTACTATTTGAT
CTATGCTGACGTGTGAGATGCGGGAATCGGCCCTGGCTCGACTCGGCCGGGCTCTGGCTGATCCGACGCGGTGCCGG
ATTCTGGTGGCGTTGCTGGATGGCGTTTGCTATCCCGGCCAGCTAGCTGCGCACCTCGGGTTGACCCGATCGAATGT
GTCCAACCATCTGTCTGTTTGGGGGGCTGCGGGCTGGTA-TCCCAACCTATGAGGGCCGGCAGGTTCCGTAT
(SEQ ID NO. 712)

.....X0015T7.seq.....
CCGCGCTGCTGCTGACGTGCGTTCGAACGTGCGACACGTCTGCGAATACCGGCCGAACGCTGGGTTTATCCACAGGCT
GGCACCAGCGCCACGACACACCGGCCGTCGCCGACCGCCACCGACTGCATCGGTTCGACGGCCATTCGGATCGCCGG
TGCCCGGGCGCTGGAACCTGGCTGGGCTGGGCTCGATGACATCGAATACGTGACCTGTATTTCGTGCTTTCCCTCCG
CTGTCCAAGTCGCCGCAATCGAACTCGGCCTGGACACCGACGATCCTGCCCGCCGCTGACCCTACCGGGGGCCTG
ACCTTCGCCGGCGGGCCGTGGAGCAATTACGTACGCACTCCAT (SEQ ID NO. 713)

Clone X0016

.....X0016SP6.seq.....
CAGGCGTGCAATGACCTGCACTGCGCCGGA-A-
TCCCTAACCCACTAAACCGGGGCCGCTCACAAGCCGTGCAGCTCGGTGAGCGTCAGGTGCGCGACCAAGGAA-
TAAATGAGCAGACCCGTGCCGTCAACGATGGTGGCGATCATCGGCCCGAAACGATGGCCGGGTC-
ATGCGCAACTTCTTCAGCAGCGCGGAAGGACGGCA-CCACCAGCGAC-ACCACACCAGAT (SEQ ID NO. 714)

.....X0016T7.seq.....

GCGAA-
CACTTCGTCAACTTCAGGGCTGCCCGCACCAAGTATTTGACGAGTATTTCCGTGCGGCCGCCGCCGCCGGCGCGC
GGCAGGTGGTCATCCTGGCGGGGGGCTGGACTCGCGCGCTACCGGCTGCCTTGGCCCCGACGGGACCACGGTTTTT
GAGCTGGACCGCCCGCAGGTCTTGATTTCAAGCGCGAGGTGCTCGCCAGCCACGGTGCCCAACCGCGCGCCCTGCG
CCGCGAGATCGCCGTGACCTGCGTGACGATTGGCCACAAGCCTTGCGGGACAGTGGTTTCGATGCGGCTGCACCGT
CGGCATGGATTGCCGAAGGGCT (SEQ ID NO. 715)

Clone X0017

.....X0017SP6.seq.....
TTGGGC-TTGGCC-CAATA-GGCCCAATCAAAGCCGAGCAGGTGGAACCTA-CGCATTGCGCTC-TCGT-
TGTGCACCCGAGCCATCGCACGCGCGGAATTCCCGAT-TC-
CCGTATTCTCCGGCGGGCGGGCTAACCCATCCCA-GCCGAACGGTTGGCTC-
TGCCGTGGGTCCCGTGTGGCCGATCGGGCGCTACCGGGGGTGCTCGGGTGCGG-TGACCATGGC-AACTGCCCC-
ATGGGCCGACCTGGTGCAGATAAACCTG (SEQ ID NO. 716)

.....X0017T7.seq.....

TGGTGGAGGTCCCCACCAA-ACCGGCCGTAACCTCTGTCACGGAAATGCGG-
CAGGCCGCGCTAGCACGTGGTATCCGCCATAAAGGTGCACCTTAAGCACGGCGTCCCAATTCTCGAACGACATCTT
GTGGAAGGTGCCGTGCGCAAGATCCCGCGTGTGCTCACCACACCGTGCACGGCGCCGAATTCTGCAAGCGCGGTCT
TGATGATGTTGCTGCGCCGTCTCGGTGGCGACGCTGTCGGTA-
TTGGCGACCGCCCGGCCCCCTTGTGCGGAAATCTCGCGACGACCTCATCGCCATCGCCGAACCGGGCGCCCCG

(SEQ ID NO. 717)

Clone X0018

.....X0018SP6.seq.....
GCCGGCCAACTGGCCGGCGGGTTGCTGTC-TCAAGGTGGGTTCCGCCACCAA-ACC-
CACTCAAGGATCGCAAGGAAAGC-
TCAAGGATGCGGTGCGGGCCGCAAGGCCGCGGTCAAGGAGGGCATCGTCCCTGGTGGGGGA-
CCTCCCTCATCCACAGGCCCGCAAGGCGCTGACCGAACTGC-TGCGTC-C-GACCGGTGACAA-
GTCCTCGGTGTCCACGTGT-CTCCGAAGCCCTTGGCGCTCCGTTGTTCTGGATC-CC-CCAAC-
CTGGCTTGGACGGCTC-GTGGTGGTCAACAAGGTGACGAGCTACCGCCGGGCATGGGCTGAACGTGA

(SEQ ID NO. 718)

Clone X0018

.....X0018T7.seq.....
CGAACCT-AATTGTCCTGTAATGCCAGCTACCAA-
GCATGGCTGGTGGCCGGGCGGTGAAGCCGGCTGCGGCACCGTCCAACTC-ATGTGGAT-
GCCGGAATGGGGATGTCCGG-ACGGCGAATCCGTA-
TTGCTTGTCCCGTGAGGCCAGGTGGATGGGGGAAGGATC-TGGTGTCCGGGATGAT-
ATGGGGCCGATGCCGCCGTTGAAGTCCACTGGATCGGGAATCGGGAATCGTGAT-CCGACGTTTCAAGCCGAAC

(SEQ ID NO. 719)

Clone X0019

.....X0019SP6.seq:.....
CTAACGGAATGAAAGCCCTGGTGGCCGT-
TCGGCGGTGGCCGTCGTCGCACTGCTCGGTGTATCTTCCGCCCAAGCTGATCCCGAGGCGGATCCCGGCCGAGGTGA
GGCCAATATGGTGGCCCCCAAGTTCCCCACGTCTTGTGATCACACCGAATGGGCGCA-
TGGGGAATTCTGCCAGCCTCCGGGTCTACCCGTCCAAGTTGGGCGTACA-
CCTCCCGCCGCTCGGGATGGCCGCTGCCGACCCGGCCTGGGCC-
AGGTTCTCGCGCTGTACCCGAAGCCGACACTGCCGGC (SEQ ID NO. 720)

.....X0019T7.seq:.....
CCGCGGGACAC-CCTC-
ATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGCTTCCGCCGCGGG
CGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTTCGATGACGGCATCGCCACCGGAGCGACGGCCAAGGC
GGCGTGCCAGGTGCCCCGGGCGCACGGTGCGGACAAGGTGGTGTGGCGGTCCCGATCGGCCCA-
ACGACATCGTGGCGAAGATTGCGCGGGTACGCCGATGATGTGGTGTGTTGGCGACCGCGGCGTTGT
(SEQ ID NO. 721)

Clone X0020

.....X0020T7.seq:.....
CTCTGGGACCGGCCACGGTGCC-
CCGGCGTTCCCGGACGTGCTGCGCCAGGTGTCCGGCGGCCGCGTGCATGGTGTTCGCGGATCGGCCGCTGGCCAGAG
CCCACCGGTGAATCTGGCCCTGGCCGACCACCGTGCGCCGTAGGCTTGCATCGTGCAGCGCTGGCGTGGCCAGGA
CGAGATCCCGACGGATTGGGGCAGATGCGTGCTCACCATCGGGGTATTTGACGGCGTGCACCGCGGGCACGCCGAAC
TGATCGCGCACGCGGTCAAAGCGGC (SEQ ID NO. 722)

Clone X0021

.....X0021SP6.seq:.....
AATACTCAAGCTTTCGTGAGTTCATTGCGCCAGCAGACCAACAA-AGCATCGGGACATACGGA-
TCAACTACCCGGCCAACGGTGATTTCTTGGCCGCCGCTGACGGCGCGAACGACGCCAGCGACCAC-
TTCAGCAAATGGCCA-CGCGTGCCGGGGCCACGAGGTGGTGTCTCGGCGGCTACTCCAGGGTGC GGCGCTGATC-
ACATC-TCACCGCCGCACCACTGCCCCGGCTCGGGTTACGCGAGCCGTTGCCGCCCGCAGCGGAC-
ATCACATCGCCGCGATCGCCCTGTTGCGGAATCCCTC-GGCCGCGCTGGCGGGCTGATTAAC (SEQ ID NO. 723)

.....X0021T7.seq:.....
TGCCGCGGATTTGGCTGGCTGCCCAATATTGAGATCGGGCCTTTCTTTTTCGCGGACAATAAGGTCACAGTAAACC
CTCGTTTGTGAGATGCGGGGCGGGGCCGGGCGAA-
TCGACCTCGAGTGAATGGATCTCGAGTGAATGGACAGGGCATCGCCTACGAGTCGCATCCCCATCCAACAGACCGGT
GCTCTGTCATCGGACCTGAAGGTCCCGCACGGAGGGTGTGGTTGCCGGCGCGGGGTACCGGTGCGGTAGCGACGTA
GTGTTGAACGAATTTCTTGATGCTCAACCTGTTGGTGTTCATCCAGTTCT (SEQ ID NO. 724)

Clone X0175

.....X0175SP6.....
AA-CTTGCGCGCTCGGCCGGGTC-AGCATCCAGCTGCTCGGCAAGGAGGCCAGCTAC-C-
TCGTCGCTATGCCAGCGGTGAGATCCGCCGGGTC-
ACGTCCGCTGCCGCGCACCGCTCGGCGAAGTGGGCAATGCCGAGCAGGCAAACATCAACTGGGGCAAGGCCGGTCGG
ATGCGGTGGAAGGGCAAGCGCCCGTCCGTCCGGGGCGTGGTGAT-AACCCGGTC-
ACCACCGCACGGCGGTGGTGAAGGTAAAACCTCCGGCGGCCGTACCCGTTAGCCCGTGGGGCAA
(SEQ ID NO. 725)

.....X0175T7.....
A-TCGAAAGTGACCATCTACCTTGAGTGCCATACCGCCGACCCATGCTCGGATAGCTCGGCGGAAAGAAACG
CTTGCACTGCCCGCAATAGCGGGTACGTCGTGAGCGCCCATCAACTCTCGCGCGGAGTGATCGCCAGCTGGGCG
GCGCCGACGTGACCGTGGGGATTCCGGTGCGCGCCGCGGCCAACGGCCCGATCGTGCACCGCACGGCAGATCGGC
GCGATGTTGTAACGCTGCATAGGCACTCCCGCGCGCTGGCAGGCCAGTGCGAACGCCCGCGCGGTGCGTCCG
(SEQ ID NO. 726)

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fragment chicken bacterial artificial chromosome library. Genomics. 42:217-226.

CLAIMS

1. A method for isolating a polynucleotide of interest that is present in a genome of a first mycobacterium strain or that is expressed by said first mycobacterium strain and that is absent or altered in a genome of a second mycobacterium strain that is different from the first mycobacterium strain or that is not expressed in the second mycobacterium strain, said method comprising:
- 5 a) contacting under hybridizing conditions the genomic DNA of the first mycobacterium strain with the DNA of at least one clone that belongs to a bacterial artificial chromosome (BAC) genomic DNA library of the second mycobacterium strain ; and
- 10 b) isolating the polynucleotide of interest that fails to form a hybrid with the DNA of the second mycobacterium strain.
2. The method according to claim 1, wherein the BAC-based DNA library
- 15 has been constructed from genomic DNA of *Mycobacterium tuberculosis*.
3. The method according to claim 2, wherein the BAC-based DNA library has been constructed from genomic DNA of *Mycobacterium tuberculosis* strain H37Rv.
4. The method according to claim 3, wherein the BAC-based DNA library
- 20 has been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on November 19, 1997 under the accession number I-1945.
5. The method according to claim 1, wherein the BAC-based DNA library has been constructed from genomic DNA of *Mycobacterium bovis*.
6. The method according to claim 5, wherein the BAC-based DNA library
- 25 has been constructed from the genomic DNA of *Mycobacterium bovis* BCG strain Pasteur.
7. The method according to claim 6, wherein the at least one BAC-based DNA library has been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on XX XX, 1998 under the accession number I-
- 30 XXXX.
8. A method of isolating a polynucleotide of interest that is present in a genome of a first mycobacterium strain or that is expressed by the first mycobacterium strain and that is absent or altered in a genome of a second mycobacterium strain or that is not expressed by the second mycobacterium strain, said method comprising :
- 35

- a) providing at least one polynucleotide contained in a clone of a bacterial artificial chromosome (BAC) DNA library of the first mycobacterium strain;
b) providing at least one genomic or cDNA polynucleotide from a second mycobacterium strain that is different from the first mycobacterium strain or at
5 least one polynucleotide contained in a clone of a BAC DNA library prepared from the genome of the second mycobacterium strain;
c) contacting under hybridizing conditions the polynucleotide of step a) with the polynucleotide of step b); and
d) isolating the polynucleotide of step a) that has not formed a hybrid complex
10 with the polynucleotide of step b).

9. The method of claim 8, wherein the polynucleotide contained in a clone of a BAC DNA library of the first or second mycobacterium strain is prepared by the following procedure :

- 1) digesting at least one recombinant BAC clone by an appropriate restriction
15 endonuclease to yield a polynucleotide insert of interest; and
2) isolating the polynucleotide insert of interest.

10. A purified polynucleotide of interest that has been isolated according to the method of claim 8.

11. The purified polynucleotide of claim 10 which contains at least one
20 Open Reading Frame (ORF).

12. The purified polynucleotide of claim 11, which is SEQ ID N0:1.

13. The purified polynucleotide of claim 11, wherein said polynucleotide is selected from the group consisting of :

- a) a polynucleotide comprising at least 8 consecutive nucleotides of SEQ ID
25 N0:1 ;
b) a polynucleotide having a sequence fully complementary to SEQ ID N°:1 ; and
c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).

14. The purified polynucleotide of claim 13, which is SEQ ID N0:2.

- 30 15. The purified polynucleotide of claim 13, which is SEQ ID N0:3.

16. The purified polynucleotide of claim 11, wherein the ORF encodes all or part of a polypeptide involved in the pathogenicity of a mycobacterium strain.

17. The purified polynucleotide of claim 11, wherein the ORF encodes all or part of a Polymorphism Glycine Rich Sequence (PGRS).

18. The purified polynucleotide of claim 17, which is SEQ ID N0:4.

19. The purified polynucleotide of claim 17, which is selected from the group consisting of :

a) a polynucleotide comprising at least 8 consecutive nucleotides the of SEQ ID N0:5 ;

b) a polynucleotide having a sequence that is fully complementary to SEQ ID N0:5 ;

c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).

20. A pair of the purified polynucleotides as claimed in claim 10.

21. A *Mycobacterium tuberculosis* strain Rv37 genomic DNA library that has been deposited in the Collection Nationale de Cultures de Microorganismes under accession number I-1945, wherein said genomic DNA library comprises recombinant bacterial artificial chromosome vectors.

22. A recombinant bacterial artificial chromosome (BAC) vector, which belongs to the genomic DNA library of claim 21.

23. The recombinant BAC vector of claim 22, which is selected from the group consisting of :

Rv101; Rv102; Rv103; Rv104; Rv105; Rv106; Rv107; Rv108; Rv109; Rv10;
Rv110; Rv111; Rv112; Rv113; Rv114; Rv115; Rv116; Rv117; Rv118; Rv119;
Rv11; Rv120; Rv121; Rv122; Rv123; Rv124; Rv126; Rv127; Rv128; Rv129;
Rv130; Rv132; Rv134; Rv135; Rv136; Rv137; Rv138; Rv139; Rv13; Rv140;
Rv141; Rv142; Rv143; Rv144; Rv145; Rv146; Rv147; Rv148; Rv149; Rv14;
Rv150; Rv151; Rv152; Rv153; Rv154; Rv155; Rv156; Rv157; Rv159; Rv15;
Rv160; Rv161; Rv162; Rv163; Rv164; Rv165; Rv166; Rv167; Rv169; Rv16;
Rv170; Rv171; Rv172; Rv173; Rv174; Rv175; Rv176; Rv177; Rv178; Rv179;
Rv17; Rv180; Rv181; Rv182; Rv183; Rv184; Rv185; Rv186; Rv187; Rv188;
Rv18; Rv190; Rv191; Rv192; Rv193; Rv194; Rv195; Rv196; Rv19; Rv1; Rv201;
Rv204; Rv205; Rv207; Rv209; Rv20; Rv214; Rv215; Rv217; Rv218; Rv219;
Rv21; Rv220; Rv221; Rv222; Rv223; Rv224; Rv225; Rv226; Rv227; Rv228;
Rv229; Rv22; Rv230; Rv231; Rv232; Rv233; Rv234; Rv235; Rv237; Rv240;
Rv241; Rv243; Rv244; Rv245; Rv246; Rv247; Rv249; Rv24; Rv251; Rv252;
Rv253; Rv254; Rv255; Rv257; Rv258; Rv259; Rv25; Rv260; Rv261; Rv262;
Rv263; Rv264; Rv265; Rv266; Rv267; Rv268; Rv269; Rv26; Rv270; Rv271;
Rv272; Rv273; Rv274; Rv275; Rv276; Rv277; Rv278; Rv279; Rv27; Rv280;

Rv281; Rv282; Rv283; Rv284; Rv285; Rv286; Rv287; Rv288; Rv289; Rv28;
 Rv290; Rv291; Rv292; Rv293; Rv294; Rv295; Rv296; Rv29; Rv2; Rv301;
 Rv302; Rv303; Rv304; Rv306; Rv307; Rv308; Rv309; Rv30; Rv310; Rv311;
 Rv312; Rv313; Rv314; Rv315; Rv316; Rv317; Rv318; Rv319; Rv31; Rv32;
 5 Rv322; Rv327; Rv328; Rv329; Rv32; Rv330; Rv331; Rv333; Rv334; Rv335;
 Rv336; Rv337; Rv338; Rv339; Rv33; Rv340; Rv341; Rv343; Rv344; Rv346;
 Rv347; Rv348; Rv349; Rv34; Rv350; Rv351; Rv352; Rv353; Rv354; Rv355;
 Rv356; Rv357; Rv358; Rv359; Rv35; Rv360; Rv361; Rv363; Rv364; Rv365;
 Rv366; Rv367; Rv368; Rv369; Rv36; Rv370; Rv371; Rv373; Rv374; Rv375;
 10 Rv376; Rv377; Rv378; Rv379; Rv37; Rv381; Rv382; Rv383; Rv384; Rv385;
 Rv386; Rv387; Rv388; Rv389; Rv38; Rv390; Rv391; Rv392; Rv393; Rv396;
 Rv39; Rv3; Rv40; Rv412; Rv413; Rv414; Rv415; Rv416; Rv417; Rv418; Rv419;
 Rv41; Rv42; Rv43; Rv44; Rv45; Rv46; Rv47; Rv48; Rv49; Rv4; Rv50; Rv51;
 Rv52; Rv53; Rv54; Rv55; Rv56; Rv57; Rv58; Rv59; Rv5; Rv60; Rv61; Rv62;
 15 Rv63; Rv64; Rv65; Rv66; Rv67; Rv68; Rv69; Rv6; Rv70; Rv71; Rv72; Rv73;
 Rv74; Rv75; Rv76; Rv77; Rv78; Rv79; Rv7; Rv80; Rv81; Rv82; Rv83; Rv84;
 Rv85; Rv86; Rv87; Rv88; Rv89; Rv8; Rv90; Rv91; Rv92; Rv94; Rv95; Rv96
 and Rv9.

24. The recombinant BAC vector of claim 22, which is selected from the
 20 group consisting of :
 Rv234; Rv351; Rv166; Rv35; Rv415; Rv404; Rv209; Rv272; Rv30; Rv228;
 Rv233; Rb38; Rv280; Rv177; Rv48; Rv374; Rv151; Rv238; Rv156; Rv92; Rv3;
 Rv403; Rv322; Rv243; Rv330; Rv285; Rv233; Rv219; Rv416; Rv67; Rv222;
 Rv149; Rv279; Rv87; Rv273; Rv266; Rv25; Rv136; Rv414; Rv13; Rv289; Rv60;
 25 Rv104; Rv5; Rv165; Rv215; Rv329; Rv240; Rv19; Rv74; Rv411; Rv167; Rv56;
 Rv80; Rv164; Rv59; Rv313; Rv265; Rv308; Rv220; Rv258; Rv339; Rv121;
 Rv419; Rv418; Rv45; Rv217; Rv134; Rv17; Rv103; Rv21; Rv22; Rv2; Rv270;
 Rv267; Rv174; Rv257; Rv44; Rv71; Rv7; Rv27; Rv191; Rv230; Rv128; Rv407;
 Rv106; Rv39; Rv255; Rv74; Rv355; Rv268; Rv58; Rv173; Rv264; Rv417;
 30 Rv401; Rv144; Rv302; Rv81; Rv163; Rv281; Rv221; Rv420; Rv175; Rv86;
 Rv412; Rv73; Rv269; Rv214; Rv287; Rv42 and Rv143.

25. A *Mycobacterium bovis* BCG strain Pasteur genomic DNA library,
 wherein said genomic DNA library comprises recombinant bacterial artificial
 chromosome vectors.

26. A recombinant bacterial artificial chromosome (BAC) vector, which belongs to the genomic DNA library of claim 25.

27. A recombinant BAC vector according to claim 26, which is selected from the group consisting of :

5 X0001; X0002; X0003; X0004; X0006; X0007; X0008; X0009; X0010; X0012; X0013; X0014; X0015; X0016; X0017; X0018; X0019; X0020; X0021 and X0175.

28. A method for detecting a mycobacterial nucleic acid in a biological sample comprising the steps of :

- 10 a) contacting the recombinant BAC vector according to claim 22 or 26, or a purified polynucleotide according to claim 10 with the mycobacterial nucleic acid in the biological sample ; and
b) detecting a hybrid nucleic acid molecule formed between said recombinant BAC vector or said purified polynucleotide and the mycobacterial nucleic acid in
15 the biological sample.

29. The method of claim 28, further comprising before step a), making the mycobacterial nucleic acid in the biological sample available to a hybridization reaction.

30. A method for detecting mycobacterial nucleic acid in a biological sample comprising the steps of :

- 20 a) contacting a first polynucleotide according to claim 10 that has been immobilized onto a substrate with the mycobacterial nucleic acid in the biological sample ; and
b) contacting a hybrid nucleic acid molecule formed between said first polynucleotide and the mycobacterial nucleic acid in the biological sample with a
25 second, labeled polynucleotide according to claim 10, wherein said second polynucleotide and said first polynucleotide have non-overlapping sequences.

31. The method of claim 30, further comprising before step a), making the mycobacterial nucleic acid in the biological sample available to a hybridization
30 reaction.

32. The method of claim 30 or 31, further comprising before step b), removing the mycobacterial nucleic acid that is not hybridized with the immobilized first polynucleotide.

33. A method for detecting mycobacterial nucleic acid in a biological sample comprising the steps of :

- a) contacting the mycobacterial nucleic acid in the biological sample with a pair of purified polynucleotides according to claim 20 ;
- b) amplifying said mycobacterial nucleic acid ; and
- c) detecting the amplified mycobacterial nucleic acid.

5 34. The method of claim 33, further comprising before step a), making the mycobacterial nucleic acid in the biological sample available to a hybridization reaction.

35. A kit for detecting a mycobacterium in a biological sample comprising :

- 10 a) a recombinant BAC vector according to claim 22 or 26, or a purified polynucleotide according to claim 10 ; and
- b) reagents necessary to perform a nucleic acid hybridization reaction.

36. A kit for detecting a mycobacterium in a biological sample comprising :

- 15 a) a recombinant BAC vector according to claim 22 or 26, or a first polynucleotide according to claim 10 that is immobilized onto a substrate ;
- b) reagents necessary to perform a nucleic acid hybridization reaction ; and
- c) a second polynucleotide according to claim 10, wherein said second polynucleotide is radioactively or non-radioactively labeled, and wherein said
- 20 second polynucleotide and said first polynucleotide have non-overlapping sequences.

37. A kit for detecting a mycobacterium in a biological sample comprising :

- a) a pair of purified polynucleotides according to claim 20 ; and
- 25 b) reagents necessary to perform a nucleic acid amplification reaction.

38. A method for detecting the presence of a genomic DNA, a cDNA or a mRNA of a mycobacterium in a biological sample, comprising the steps of :

- a) contacting the biological sample with a plurality of BAC vectors according to claim 22 or 26, or purified polynucleotides according to claim 10 that are
- 30 immobilized on a substrate ; and
- b) detecting the hybrid complexes formed.

39. A kit for detecting a genomic DNA, a cDNA or a mRNA of a mycobacterium in a biological sample, comprising :

- a) a substrate on which a plurality of BAC vectors according to claim 22 or 26, or
- 35 purified polynucleotides according to claim 10 have been immobilized.

40. A method for detecting a polynucleotide of mycobacterial origin in a biological sample, said method comprising :

- a) aligning at least one polynucleotide contained in a recombinant BAC vector according to claim 22 or 26 on the surface of a substrate ;
- 5 b) contacting the polynucleotide in the biological sample with the substrate on which the polynucleotide of step a) has been aligned ; and
- c) detecting a hybrid nucleic acid molecule formed between the polynucleotide in the biological sample and the aligned polynucleotide of step a).

41. A kit for detecting a polynucleotide of mycobacterial origin in a biological sample, comprising :

- 10 a) a substrate on which at least one polynucleotide contained in a recombinant BAC vector according to claim 22 or 26 has been aligned.

42. The method of claim 9, wherein the procedure by which the polynucleotide contained in a clone of a BAC DNA library is prepared, further
15 comprises amplifying the polynucleotide insert.

43. The method of claim 9, wherein the procedure by which the polynucleotide contained in a clone of a BAC DNA library is prepared, further comprises digesting the polynucleotide insert with at least one restriction endonuclease.

20 44. The method of claim 42, further comprising digesting the amplified polynucleotide insert with at least one restriction endonuclease.

45. The Polynucleotide of claim 16, wherein the mycobacterium strain is *Mycobacterium tuberculosis*.

25 46. The method of claim 33, wherein the amplified mycobacterial DNA is detected by gel electrophoresis or with a labeled polynucleotide according to claim 10.

47. The kit of claim 37, further comprising a polynucleotide according to claim 10.

30 48. The kit of claim 39, further comprising reagents necessary to perform a hybridization reaction.

49. A method for physically mapping a polynucleotide of mycobacterial origin in a biological sample, said method comprising:

- a) aligning at least one polynucleotide contained in a recombinant BAC vector according to claim 22 or 26 on the surface of a substrate;

- b) contacting the polynucleotide in the biological sample with the substrate on which the polynucleotide of step a) has been aligned under hybridizing conditions; and
 - c) detecting the location of the hybridized polynucleotide from the biological sample.
- 5

50. The kit of claim 41, further comprising reagents necessary for labeling DNA and reagents necessary for performing a hybridization reaction.

CCTTCTACGCCCCGATCTCGCCGGAACCGTTGTGCTGGTGGGTGTTCCNACGCCCCGACATGCGCCTGGACATGCCGC
TGGTCNACTTCTTCTCTCACGG (SEQ ID NO. 458)

.....Rv349T7.seq:.....
TCGACGGTTTGGCGGCCTTAAATGCACTGAGGTCGTCAATTGACCCACAGCGGAAATGCCGACTATTGCGAGGCCTC
CTTCGCCTTGGCTGCCGAGAGGGGCTCCGCGGGAACCGCATGCAGGTATATGACCTCGGTTTCTCGGGTGCTACCGC
GTGCCTTGTNTANGATNANCTCGGCGTTGGAATTGTCCAGCCGCGCCAATTCATCGAGCGCANATTCTGACACNTGGC
CGGCGGCACATACGCTTCACCGTGGATCTGCTCCACAGGACCGCCCTGTCCGGATCCTGCTCACGGTAANGGAAC
TTACGTGGCACTCGG (SEQ ID NO. 459)

Clone Rv34

.....Rv34SP6.seq:.....
GACCACGCCAGGCTAATCACGTGACGCTACCGAATACCCTNCCTAGTGGTGCAGGCTCCCGCTGGAAATGGCCCTGTA
CCAACTCGCGCACCGGTGCCAG (SEQ ID NO. 460)

.....Rv34T7.seq:.....
CGGCACCCGACCCCTTTGAGCCGTCCGCCGTGGCCGCGGTGGAACCTGGCCGACGAGGGACTGATCGTGCTGGGCAAAT
TGGTCGATGGCACGCTGGCCGCCGATCTGAAGGTCN (SEQ ID NO. 461)

Clone Rv350

.....Rv350SP6.seq:.....
CTCAAGCTTGCCGTTACCCGACTTCCGGAGGGACACCATGAGCACCGCCAGCCGAGCACGAGGGCCAAACTCCGCCGA
CGCAGCGCGGTTGGACTTGTGCTGCTGGACAAGGGGTTAGCCGCCGAAGCAGTGACGTACATCGGCGAAAAGCAGTT
CGCCTGTGACACCGACGGNGCANNACCGTGAGGCTAGGGAAGCGAGGAGCACATGGCCGCCGACCGCAATGTACACGCT
GCAAGCAAACCATCGAACC CGGATGGCTATNCNTCACCGCCCATCGCCGCGGT (SEQ ID NO. 462)

.....Rv350T7.seq:.....
CATGTGCGGCACATCCAGGACTTCTGGGGGGATCCGCTGACAGCGGCGGGATCCCAAAGTGCGGATGATCGGGCCGCC
TACGTCGTGGTGTAACCTCGGTAAACAACGAAACCGAAGCGTATGACTCGGTCCACGCGGTGCGGCACATGGTGGAC
ACCACACCGCCACCGCACGGGGTGAAGGCCTATGTCAACCGTCCGGCAGCACTCAATGCCGACAGGCGGAGCCGGA
GACAAAAGTATCGCTAAGGTCACCGCGATCACGAGCATGGTGATCGCAGCAATG (SEQ ID NO. 463)

Clone Rv351

.....Rv351SP6.seq:.....
ATACTCAAGCTTCGGTACGGTGGCGGGCGGTGCTGCTGGCCGCGGTGCGGGCGGTGCGGGCGCTGCGGTCTCGTTTACN
AGCTCGCGCTGCTGACACTGGCGGCNAGCCTGAACGGCGGCGGGATCGTGCCACCTCCCTGATCGTCGCGGGCTACA
TAGCCGCGCTGGGAGCAGGCGCCTTGCTGATCAAGCCGCTACTTGACACGCGGCCATCGCGTTCATCGCCGTGGAGG
CGGTGCTGGGCATCATCGGCG (SEQ ID NO. 464)

.....Rv351T7.seq:.....
TGTCAGTCCTTTCAGATCTCNTTTTATGACATGACTGGAGATCTGTCTAGATTGCACTCCTGTGAGCGTGGGTAC
CGGATTCAAGCCGGTCGGTCACGCCGCGGTGGTACCGGCTTTGCGGCAGTGCTCGGCCTCGAGTTCGGCGATCGCGCG
CGAAGTGCGTTCGCGCAGCAAGATCGCGGCCGTAATGCCGGCGATGACCGCGATGACCAGCGCGATCCAGGAGAACCG
TTCCAACCACTGCTGGGCGGCCATCCCGGCGAAGTAGACCAGTGCACTGGTGCC (SEQ ID NO. 465)

Clone Rv352

.....Rv352SP6.seq:.....
CAATACTCAAGCTTCAAACAGGCCTGTTGTGGGCGCAACCGGCTCGCCGAGTTCTGCACGCACCGCCTCAANTGCGG
CCCGCACCGCCGGCATCTCCCGGTACGCAGGGCCGCGGCCCGCGCCGANCAGCGNGTGTTCCGCGCAGTTTCGCCGT
CAATGATGCTGACCTGATCGGCCACCCGGCGGTTCTCGGCGTCTGTCGTTCACTAATCGCGGTGCTC
(SEQ ID NO. 466)

.....Rv352T7.seq:.....
TACGTGGCGCTGGAGGGAGCCANNACAAATCCACGCCAATGCTCTTGCCCCGATCGCGGCGAGCCAGGATGACCCA
GGACATCCTGCCGCCCCAAGTACTGGAAAAGCTCACACCCGAGTTCGTGCGACCGGTGGTGCCCTACCTGTGCACCGA
GGAGTGTGCCGACAACGCATCGGTGTACGTGCTCGGTGGTGGCAAGGTGCAGCGAGTTGCGCTGTTTGGCAACGACGG
CGCCAACCTCGACAAACCGCGTGGTACAAGATGTTGCGGCGCGGTGGGCGGAGATCACCGATCTGTCCGGTGCGAA
AATTGCTG (SEQ ID NO. 467)

Clone Rv353

:::Rv353SP6.seq:::

GCTTTTCCCGTCCGTCNNCGCTCAACCGCGTGAGGCCGAAGCGGNTGGTTACGACTCCCTGTTTGTGATGGACCACTT
CTACCAACTGCCCATGTTGGGGACNCCCGACCAAGCCGATGCTGGAGGCCCTACACGGCCCTTGGTGCGCTGGCCACGGC
GACCGANCGGCTGCNNNTGGGCGCGTTGGTGACCGGCAATACCTACCGCAGCCCGACCCCTGCTGGCAAANATCATCAC
CACGCTCGACGTGTTAGCGCCGTCGAGCGATCCTCGGCATTGGAGCCGGTGGTTTGANCTGGAACA

(SEQ ID NO. 468)

:::Rv353T7.seq:::

CNGCTTTTAAATGGCCTTGACNTGGGCGNGCCGGCCACCGGGGCCACTCCGCACAATCTGTACCCGACCAAGATCTAC
ACCATCGAATACGACGGCGTCGCGGACTTTCCGCGGTACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGC
ACCTACTACGTGCACTCCAATACTTTCATCCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTC
GGTCCCACGATGACCCAGTACTACATCATTGCGACGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATC
GTGGGAACCACTGGCGAACCTGGTTCAACCAAACTTGAAGGTGATTGTAACTGGGCTACGGCGACCCGGCCTAT
G (SEQ ID NO. 469)

Clone Rv354

:::Rv354SP6.seq:::

CTCAAGCTTGCCGGGAGGGTGATGGCCGACTCGGATTTACCCACCANGGGGCGCCAACGCGGTGTCCGCGCCGTCNA
GCTGAACGTTGCTGCCCGCTGGGAGAACCTGGCGCTGCTGCGCACCTTGGTGGCGGCCATCGGCACCTTCGAGGACCT
GGATTTGACGCGCGTGGCGGACCTGAGGTTGGCGGTGGACGAGGTGTGCACCCGGTTGATTGCTCGCTCGGCCTTGCCGGA
TGCCACCTGCGCCTGGTGGTGCATCCGCGAAANACGAANTTGTGGTGGAGGCTTCTGCTGCCTGCGACACCCACNA
CGTGGTGGCACCGGCGAGCTTAGCTGGCAT (SEQ ID NO. 470)

:::Rv354T7.seq:::

CCGACGCCGTCGTGGCCACCAACACCGCGACCGAGCACCCTGACCCGGACCGGGGTGCCGCGGAACCGGTCTTGCCA
ATTGCCGCGGCCACCAAGCCGTCGCGGCCATGGCGAACAGCAGCGCGCATTGCCCGAGCATCAACACCATCACCACCG
TGGTAAGCCCGGCCAGCGCGCCGACGAGATGATGCCGCTGGCCAGTACACCCGTTGGCCTGGAACGCGGTGGCCA
GATTTGCCGGCCCGCGGCCCGGTACGGTCCGAGTTGGGTGTATGGAACCATGCCCGACGACCAACCG

(SEQ ID NO. 471)

Clone Rv355

:::Rv355SP6.seq:::

TTNACTGGCCTTGGTCCACACTAGACAATACTCAAGCTTCCAGGACATCGTCATCGCGACCAAAACCGCGAGCTAGG
TCGGCATCCGGGAAGCATCGCGACACCGTGGCGCCGACGCGCGCTGCCGGCAGGCCGATTAGGCGGGCAAATTAGCCC
GCCGCGGCTCCGGCTCCGANTACGGCGCCCCGAATGGCGTCACCGGCTGGTAACACGCTTGCGCGCCTGGGCGGGC
GCCTGCCGGATCAGGTGGTAAATGCCGACA (SEQ ID NO. 472)

:::Rv355T7.seq:::

NGACGCTTCCATCCGCGCGTCGTTTTGGCGGGTTGGCCACAGCAGCCCGCGGTGACGGCGACGATGCTGGGCTGGT
TGCGGCCCTGCGCCACCGCGGCTTGATGCTGGTTGGCTGTCTTGGGACGATCCCGAAATAGTCCACGCGGATCTGGT
GATTTTGGGGCTACCCGCGATTACCCGCGCGGCTCGACGAGTTTTTGGCCTGGACTACCCGCTGGCCAATCTGCT
GAACGCGCGCGGTGGTGGCCTGGAATGTCGAGCGCGGTACCTA (SEQ ID NO. 473)

Clone Rv356

:::Rv356SP6.seq:::

CTTCTCTGAGTACCNCCGNTACTTTGGGATGGGTAAAAAGGCGAATCNCCTTTGGTCACGAACGCCGGGAGGG
ACAATCTCGGGCGGCTGGGGCCTCTCGGGGAANGCCCGAATGTACGGTGTCTCGACACTTCCNTCCCCCTCCG
(SEQ ID NO. 474)

:::Rv356T7.seq:::

GAGCATCGGGACNTACGGAGTCACTACCCGGCCAACGGTGATTTCTTGGCCGCCGCTGACGGCGCGAAGCAGCCNG
CGACCACATTGACGAGATGGCCAGCGCGTGCCGGGCCACGAGGTTGGTGTCTCGCGGCTACTCCAGGGTGCGGCCNT
GATCNACATCGTCACCGCCGACCACTGCCCGGCTCGGGTTACGCGAGCGGTTGCCGCCNCAGCGGACGATCACNT
CGCCGCGATCGCC (SEQ ID NO. 475)

Clone Rv357

:::Rv357SP6.seq:::

TACTCATGANCATCCTTTAATCANNGCTTTGCGTTTTTTATTAAATCTTGCAATTTACTGCAAAGCAACAACAAAT
CGCAAAGTCATCAAAAACCGCAAAGTTGTTTAAATAAGAGCANCACTACAAAAGGAGATAAGAAGAGCATACCT

CAGTCACTTATTATCACTAGCGCTCGCCGAGCCGTGTAACCGAGCATAGCGAGCGAACTGGCGAGGAAGCAAAGAAG
AACTGTTCTGTGATAGCTCTTACGCNCA (SEQ ID NO. 476)

Clone Rv358

.....Rv358SP6.seq:.....
CTCAAGCTTCAGGTCAATGTGCNCCAAGCCCTGACGCTGGCCGACCAGGCCACCGCCGCGGANACNCTGCCAAGGCC
ACCGAATACAACAACGCCGCCGAGGCGTTTCGCANCCAGCTGGTGACCGCCGAGCANANCGTCAAAAACCTCAAGACG
CTGCATGACCAGGCGCTTANCCCGCANCTCAGGCCAAGAAGGCCGTCNAACGAAATGCGATGGTGCTGCACCANAAG
ATCGCCGAGCGAACCAAGCTGCTCAGCCNG (SEQ ID NO. 477)

.....Rv358T7.seq:.....
CATGGTGGCACTGTAGCGACGTGCTGCAATCAAGGTCATGCCGACTCTGGTCAGCTCGGANCCGCTGACACCCCGCT
AAGGCTGCTCAGCTCGGTGCATTACCTCACCGACGGCGAACTCCCCAGCTTTACGACTATCCGGATGACGGCACCTG
GTTGCGGGCGAAGTTTCATCATCAGCTTGGACGGCGGCGCTACCGTCGATGGCACCAGCGGGCGATGGCCGGGCCCGG
CGACCGATTTCGTCTTCAACCTGTTGCGTGAAGTTGCCGACGTCATCGTGGTCGGCGTGGGCACCGTGCGCATTGAGGG
CTACTCCGGCGTCCGGATGGGTGTCGTCCAGCGCCAGCAC (SEQ ID NO. 478)

Clone Rv359

.....Rv359SP6.seq:.....
TACTCAAGCTTGCGGGTGATCGCCTTGGTCAACGGCACCGTGATCGGATCGGGGTCNACCGCACAAATGGACTGGAGC
TTCGGCGAANTCATCGCCTATGCCTCGCGGGGGTGACGCTGACCCCGGTGACNTGTTCCGGCTCGGGCACGGTGCCC
ACCTGCACGCTCGTCTATCACCTCNGGCCACCGGAATCATTCCCGGGCTGG (SEQ ID NO. 479)

.....Rv359T7.seq:.....
GTTGGNGCCTCGTCGGCGAACAGTTCTCGCACGATTTCCGGATTAGCGGGACTGGTCACCAAGTTGGGTATGCGGGAAG
GCGCTGACGTTTCGCCGCGATTAGCTGTTTGATGGACGCGGTGGTGATGTTCTGATCACGGAAGTTGGCTGTAATAGCCC
AGGGTCGCCACGCTTTCATCCGGGCCCGGACCGGGCGCACCGAGCGTGTCGCGCAGGTATGCGACGTGATTTTCGCTG
AAGTCCCCGTACCCGGAGAACT (SEQ ID NO. 480)

Clone Rv35

.....Rv35SP6.seq:.....
TGCTTCCGGCTCGTATGTTGTGTGGAATTGTGANCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG
CCAAGTATTTAGGTGACACTATAGAATACTCAAGCTCCAGGTCAATGTGCGCCAAGCCCTGACGCTGGCCGACCAGG
CCACCGCCGCCGAGACGCTGCCTTTGTACCCGAATACAACAACGCCGCCGAGGCGTTTCGACGCCAGCTGGTGACCG
CCGAGCAGAGCGTCGAAGACCTCAAGACGCTGCATGACCAGGCGCTTAGCGCCGACGCTCAGGCCAAGAATGCCGTCG
AACGAAATGCGATGGTGTCGCGGCATAAGATCGCCGAGCGAACAAGCTGCTCAGCCAGCTCGAGCAGGCGAAGATGC
ACGAGCA (SEQ ID NO. 481)

.....Rv35T7.seq:.....
CAGGCATGCAAGCTTCGGAGGCGAGCCCGTGATGGTGGCACTGTAGCGACGTGCTGCAATCAAGGTCATGCCCGACT
CTGGTCAGCTCGGAGCCGCTGACACCCCGCTAAGGCTGCTCAGCTCGGTGCATTACCTCACCGACGGCGAACTCCCC
AGCTTTACGACTATCCGGATGACGGCACCTGGTTGCGGGCGAACTTCATCAGCAGCTTGGACGGCGGCGCTACCGTCG
ATGGCACCAGCGGGCGATGGCCGGGCCCGGCGACCGATTTCGTCTTCAACCTGTTGCGTGAAGTTGCCGACGTCATCG
TGGTCGGCGTGGGCACCGTGCGCATTGAAGGCTACTCCGGCGTCCGGATGGGTGTCGTCCATCGCCA
(SEQ ID NO. 482)

Clone Rv360

.....Rv360SP6.seq:.....
TACTCAAGCTTGGGGTGGCGCTGTGCGTGGTGCTTGGCGGCGTCGGTATCAACACCGCCCACGAAATGGGGCACA
AGAAGGATTTCGTGGAGCGGTGGCTGTCCAAAATCACCTCGCCCANACCTGCTACGGGCACTTCTACATCGAGCACA
ACCGTGGCCATCAGTCCGGGTGTCCACACCGGAGGACCGGGCGTCGGCGCGGTTCCGGCNAACGTTGTGGGANTTCC
TGCCCCGCANTGTTATCGGCGGCTTGCCT (SEQ ID NO. 483)

.....Rv360T7.seq:.....
GGCCATCGCCACCGCNCGGCGGAACGCTCAAAGGCACCTACTGGCACCAAGGCCCCACACGTCACCCCTGTGACCTC
CTGCGCCGACCCGCCCGAGGTCTTGGCCGTTACCACCGAACGGGCGAGCCGGGAGTCTGGTACGCATCGAACAAGA
GCAAGGTGCATGGGCGGAGTTGTTCCGCCACTTCGTGATGACGGGGTCGATCCATTGAGGTCCGTGCGCCGCTCGG
TCGAGTGGCGGTCACTCCANGTACTCGACCTCACAGACGAGAGGACTCGATCCCATCTAGGTGTGGACGAAACAGA
TCTTCTGTCCGACGACTACACCACCCAGGCCATCGC (SEQ ID NO. 484)

Clone Rv361

.....Rv361SP6.seq.....
GCTTGGCGGTGATCGCCTTGGTCAACGGCACCGTGATCGGATCGGGGTCNACCGCNCAGATGGACTGGANCTTCGGCG
AANTCNTCGCCTATGCCTCGCGGGGGGTGACCTGACCCCGGGTGACNTGTTGGGCTCGGGCACGGTGGCCACCTGCA
CGCTCGTCAAGCACCTCNGGCCACCGGAATCATTCCCGGGCTGGCTGCACNACGGCGACNTGGTCNCCCTCCAGGTCG
AAGGGCTGGGCNAAACAANGCAGACCGTCCGGACAANCGGCACTCCTTTCCGTTGGCTCTTCGGCCGAATCCGGACG
CCNAACCCGACCGCG (SEQ ID NO. 485)

.....Rv361T7.seq.....
GTTCTCGCACGATTTCGGATTAGCGGGACTGGTCACAGTTGGGTATGCGGAAGGCGCTGACGTTGCGCCGATT
GCTGTTTGTATGGACGCGGTGGTGTGNTGATCACGGAAGTGGCTGTAATANCCAGGGTCGCCNCGCTTTCATCCG
GGCCCGGACCGGGCGCACCGAGCGTGTGCGCGAGGTATGCGACGTGATTTTCGCTGAAGTCCCGGTACCCGGAGAACT
CGAACACGCTGAGGCGCTCGTCACCGTCGTNNCGGCGACCAAGCGCGGAGCAACTGCGCAAAATCGTTAAGANAGG
TCGAATCGTTGAAATTGCGCACCACTGCACC (SEQ ID NO. 486)

Clone Rv363

.....Rv363SP6.seq.....
CACAAACAATACTCAAGCTTCAGGTCAATGTGCNCCAAGCCCTGACGCTGGCCGACCAGGCCACCGCCCGGANAC
GCTGCCAAGGCCACCGAATAACAACGCCGCCGAGGCGTTGCGAGCCAGCTGGTGACCGCCGAGCANANCGTCNAA
AACCTCAAGACGCTGCATGACCAGGCGTTANCGCCNCAGCTCAGGCCAAGAAGGCGTCGAACGAAATGCGATGGTG
CTGCAGCANAANATCGCCGANCAACCAAGCTGCTCAGCCAGCTCGAGCAG (SEQ ID NO. 487)

.....Rv363T7.seq.....
CCACCCGTGCATGGTGGCACTGTAGCGACGTGCTGCAATCAAGGTGATGCCCCGACTCTGGTCAGCTCGGAGCCGCTGA
CACCCCGCTAAGGCTGCTCAGCTCGGTGCATTACCTCACCGACGGCGAACTCCCCAGCTTTACGACTATCCGGATGA
CGGCACCTGGTTGCGGGCGAACTTCATCAGCAGCTTGACGGCGGCGCTACCGTCGATGGCACCAGCGGGGCGATGGC
CGGGCCCGGGCGACCGATTGCTCTTCAACCTGTTGCGTGAACCTTGCC (SEQ ID NO. 488)

Clone Rv364

.....Rv364SP6.seq.....
GCTTTCCGCCGATACCCNCCATGTCCCGCACATCCAGGACTTCTGGGGGATCCGCTGACAGCGGCGGGATCCCAAAG
TGCGGATGATCGGGCCGCTACGTGCTGGTGTACCTCGNCGGTAACAACGAAACCGAANCGTATGACTCNGTCCACGC
GGTG (SEQ ID NO. 489)

.....Rv364T7.seq.....
CAACCCGANTTGGCTTTCGGCGCCNTCGGTGAGGACGGCGTGCGGGTGCTCAACGACGACGTCGTCGCGGGACACAC
CTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGATCTACNACGCCGNGNGGAACGCTTCNGCCGC
GGGCGTGACCGCNTCCCGTT (SEQ ID NO. 490)

Clone Rv365

.....Rv365SP6.seq.....
GGGATGGGCAAAAAGGCGAAGCACCGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGGCTAGGGCTTCTCGCG
GGAAGGCCCGAAGCTACGGCGTTTCAACACGTGCGCTCGCCCTCCGACCGCGAACATTGCGGGATGGCAGCAACCTGG
TAGCACCTGGCCGGGCGATGATCTGCCAGCGTCCCGCGGGTAGTCGCCGCCCGGGCGG (SEQ ID NO. 491)

.....Rv365T7.seq.....
CAGCAGACCAACAAGAGCATCGGGACATACGGAGTCAACTACCCGGCCAACGGTGATTTCTTGCCCGCGCTGACGGC
GCGAACGACGCCAGCGACCAATTGAGCAGATGGCCAGCGCGTGCCGGGCCACGAGGTTGGTGCTCGGCGGCTACTCC
CACGGTT (SEQ ID NO. 492)

Clone Rv366

.....Rv366SP6.seq.....
CTCAAGCTTGACTGGCCACCCACCGGCATGACCACCGACAGGCCCGACTGGTTCGTACCACTCGAACGCCGGGGTGT
GA (SEQ ID NO. 493)

.....Rv366T7.seq.....
TTGGTGCCCGGAATGGCGAGTCCCATTTANTCGCTGATTTGTTTGAACAGCGACGAAACCGGTGTTGAAAATGTGCGC
TGGGTGCGGGATTCCCTCTCCAAGCAAGAGTAACTGGCCCCAAATAAAGTTACTCGTCGTCTTGCAAAGACCGCTACC

CGATGCCATTTATGTGTTTCCTTACGCTCNNNNNTCCGGTGCGCCATCATTATCTGCACCTTTGCACTGCACATTGAG
CTTAGCAGCGCTCG (SEQ ID NO. 494)

Clone Rv367

.....Rv367T7.seq:.....
GAATTNGCTTTTCGGCGCCATCGGCCAGGACCGCGTGCGGGTGCTCAACGACGACGTGCTCCGCGGGACACACCTCGA
TGCTGCCGCCATGGACGCGGTGGAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGCTTCCGCCGCGGGCG
TGACCGCATCCCGTTGACCGGGCGGATCGCNGTGATCGTGCATGACGGCATCGCCACCGGAGCGACGGCCAAGGCGGC
GTGCCAGGTGCGCCGGGCGCACGGTGCGGACAAGGTGGTGCTGGCGGTCCCGATCGGCCAGACGACATCGTGGCGAG
ATTCGCCGGGTACGCCGATGAAGTGGTGT (SEQ ID NO. 495)

Clone Rv368

.....Rv368SP6.seq:.....
TAAAGCTTTCGTGAGTTCATNGNGCCCCGGACCAACAAAAGCATCGGGACATACGGAGTCAACTACCCGGCCAACGG
TGATTTCTTGGCCGCGCTGACGGCGCNAACGACGCCAGCGACCACATTCAGCAGATGGCCAGCGCGTGCCGGGCCAC
GAGGTTGGTGCTCGGCGGCTACTCCAGGGTGCGGCCGTGATCNACATCGTACCGCCGCACTACTGCCGGCCTCGG
GTTACGCGACCGGTTGCCGCCGAGCGGACGATCACNTCGCCGCGATCGCCCTGTTCCGGGAATCCCTCGGGCCGCGC
TGCGGGGCTGATGAGCGCCCTGACCCCTCAATTCCGGGTCCAANACCATCNACCTCTGCAACACGGCGACCCGATTG
TTCGGACGGCAACCGGTGGCGANCGCACCT (SEQ ID NO. 496)

.....Rv368T7.seq:.....
CCGGGAGGGACCATCNCGGCGGCTNCGGCTTCTCTCCGGAAGGTTCTANNGTNNNGCGTTTCNACNCTTCCCGTCGC
CCTGCGACCGCGGAACATTCGGGGTATGGNNGCANCTGTNAGCATCCNGGCCGGG (SEQ ID NO. 497)

Clone Rv369

.....Rv369SP6.seq:.....
CTCAAGCTTCCGCATCAGATCGCTATAGAACCAGGTGCGCGTCCCCACCGAGTGGCTGGTTCGCTTCCAGCACGATCGT
TACCGGTTATCGGAATCAAACCTCNCGAACACCTGACCAACGCGCTTGATCGCCTGAATCGATGCGGCGTCGCTGGG
GCTCATCGATACCGAGTGTGCTTTTCCGACCACTTCCAGTTGCGGTACGGCGAGATTGACAAAGGCGGTGAAGCCAG
CCAGAGCAGGACGATCACCNCCGAAACCGGCGGATTTGCCCG (SEQ ID NO. 498)

.....Rv369T7.seq:.....
GCTTGGCAGCCTGCGGCTGGGCGCCCTNGAGCTCTTCGATCTGGATCTCCGACTCGAGATGCTCACTTGCCCCGGCCG
TGGACGTACCCATTGCGGCCGGGACCCAGCGCCCGAGGTGACCAGCGAGTTGGGCTGCACGCTGACCGGCCGTCGCG
GGTCGACGCCGGTAACGGTCAGCAGCTCCGANCTCANNCTGATCCCGACCGCAGCTGCCAATGCGCGGCTGGCAGCCG
ACGTGGATGTGCCGGGGCTAGATCGCGGGGACGAGCGAGACCGGTCACCGACGGTCATCACCTTGCCGAGTTTNG
GCCTGCCCGAN (SEQ ID NO. 499)

Clone Rv36

.....Rv36SP6.seq:.....
GCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTNCACACAGGAAACAGCTATGACCATGATTACGC
CAAGCTATCTAGGTGACACTATAGAATACTCAAGCTTGAGCCATCGGGCTATCAGCTGGTTGATGTCCCG
(SEQ ID NO. 500)

.....Rv36T7.seq:.....
CAGGCATGCAAGCTTGTGCTCTATCACATCCGACCACCAACCGCCCGACGGCTCGGCAGAACGCCTCCGCATATGGGT
CGACGACGAGCGGGTCGGACTTCTGGGCTGCCAGCGCTCGCGCCGTCGCGACAAACAGCGCGGTGGAACCGACACTCC
TTGTGATGTCCACCTATCACCTTCGGTACGCACCCAATCGACCTACGCGGCTAGCTCAGCCCCGATCTTCCAGAGC
TCCGCCCG (SEQ ID NO. 501)

Clone Rv370

.....Rv370SP6.seq:.....
GCTTTTTGAGCGTCGCGCGGGGCGGCTTCCCCGGCAATTCTACTAGCGAGAAGTCTGGCCCGATACGGATCTGACCGA
AGTCGCTGCGGTGCAGCCACCTCATTTGGCGATGGCGCCGACNATGGCGCCTGGACCGATCTTGTGCCGCTTGCCGA
CGGCGACGCGGTAGGTGCTCAATTCCGGTCTACGCTTGGGCTTTGCGGACGGTCCCGACGCTGGTTCGGGTTG
(SEQ ID NO. 502)

.....Rv370T7.seq:.....
CGANCTGTTTCGACGGCTACCTGAATCACCCGATNCCACCGCCGCGGCTTCGACGCCGACAGCTGGTACCGCACCG
GCGACGTCGCGGTGGTCGACGGCAGTGGGATGCACCGCATCGTGGGACGCGAGTCGGTCGACTTGATCAAGTCGGGTG
GATACCGGGTCGGCGCCGGTGAAATTGAAACGGTGCTGCTCGGGCATCCGGACGTGGCGGAGGCGGCAGTCGTGGGG
T (SEQ ID NO. 503)

Clone Rv371

.....Rv371SP6.seq:.....
NAAGCTTTGTACACCAAGTGTTCNACCAGNCGTCCATCCGGCGAAGTGGATACTCCAGCAGGTAGCAGGTGCGC
ACCACGCTGGTCAGTGCGCTTCAGCTCGCTTGGCGGCTGCAGCAGCCAGTCCGGGAAATAGCTGCCCTGGCG
(SEQ ID NO. 504)

.....Rv371T7.seq:.....
CGCTGGNCGCCGGCGCTGGGCTGCGGTAACCAATTACCACAACACTTTTCGGTAGCCGAACAGCGGCGGTACCGCG
AAATGGCACAGCCACCGCAGTCGCGGACATCCGCGAAGATGTGGCAGATTTTCGTGCGGTGAGCCGGCGAAGGCCT
AGCGTCATTGTTGCCTGGCAAGTTGCTGGGCCCCG (SEQ ID NO. 505)

Clone Rv373

.....Rv373SP6.seq:.....
CTCAAGCTTCTTCTGCCCTTGCCGTTNCGGATNACATCCCGCAGCGACTCGGCTTCGGCGTCGATGTCGAAGTTCTC
GATCAGCTTCTGGATCGACTCCGCGCCATGGCACCAGTGAAGTACTCGCCGTAGCGGTGACNAGTTCGCGGTAGAG
GTTTCGTGTCNACNATCAGCTGCTTGGGCGCCANCTTGGTGAAAGTGCTCCAAATGTCCTCCAACCGGTCCAGCTCAGC
CTGCGCGCGGTACGGATCTGGCGCATCTCGCGCTCGCGCCGTGCGGAACCTGCGCCGCGCATCGGCCCTTGGGCCCC
(SEQ ID NO. 506)

.....Rv373T7.seq:.....
GTTACACCTACCTACTATGCCNCAATTCNCCGACAGGGTGGCATCAACACGGGCGATAAGGTGGAATCGCTGGGG
TGAACGTCGGGCTGGTGCGCTCGCTGGCAATCCGCGGCAACCGCGTGTGATCGGATTCTCGTTGCCCGGCAAGACAA
TCGGGATGCAAAAGCCGGGCGAGCAATTCNCCNACACCATTCTTGGCCGTAAGAACCTGGAGATCGAACCCCGCGGTT
CGGAGCCGTTGAAACCCAACGGTTTCTGCCGTTGGCGCANACCACTACGCCATACCAATC (SEQ ID NO. 507)

Clone Rv374

.....Rv374SP6.seq:.....
CTCAAGCTTTACGCGGACGCCGGCTACACAACACCAAGGAAACGATTGCCTACTGCCGAATCGGGGAACGGTCTCTCG
CACACCTGGTTGCTGTTGCGGGAATTACTCGGACACCAAAACGTCAAGAACTACGACGGCAGTTGGACAGAATACGGC
TCCCTGGTGGGCGCCCCGATCGAGTTGGGAAGCTGATATGTGCTCTGGACCC (SEQ ID NO. 508)

.....Rv374T7.seq:.....
TCCNCATGGGATAACGGGTTTAGATTTNACAACGGCACCGTGTTTCTCAACAAGCCGGTCATCAGCTGGGCCGGCG
ACAACGGTATCTACTTCACCCGCTTCGCCCCGTACAAGAAAAACCACTAGGCCACCATCGAGTCCAAGAACCAACC
TGGTCCGCAAGTACGCGTTCTACTACCGCTATGACACCGCGGAGGAACGCGCCGTGCTCAACCGGATGTGGAAGCTGG
TCAACGACCGCTCAACTACCTCACCCGACCATCAACCGATC (SEQ ID NO. 509)

Clone Rv375

.....Rv375SP6.seq:.....
CTCAAGCTTGGGTGTTGCCGATCACCGGAAGCCNATGATCAGCCACGTTTCGCGCCGCCCGGCATACGGCGGCGTAC
CGATCTCCGCGTCATACACCCGCGGTAATCGCCGACGGTGCCGTTTCGCGAGCCGAAGGTGACAACGCTGATTGAAT
CNAGTTCANGTCCAGCGGT (SEQ ID NO. 510)

.....Rv375T7.seq:.....
TNAACAGCTCGCGGCAGCCACGACCTGCTGCGTGGATTGCCGGCGGCGAGATCAATTCCAGGCAGCTCCCGGACAA
TGCGGCTCTGCTGGCCGCAACGAANGACTCGAGGTCAACCCGGTGCCCGGGGTGCTGGTGCACTGCCGATCGCACA
GGTTGGCCCAACAACCGCCGCTTGATGNNNGTCGGCAAGCCCGGCAGTNGCCAAACCCAGCGTGATCANGCTCGGCT
CGCGAGTTCGGCGAANAAGTGGCTCGCTGATCACCTACCATCGGCCANGATCTGCGTGTCA (SEQ ID NO. 511)

Clone Rv376

.....Rv376SP6.seq:.....
GCCANCCGGCTTGGCGTCGACTCCCGTTCNGCACATCATACGGTCCCCGGTACTGTCCAACGCGCCGGTGGCGTAGC
CAAACGTACGACTCTCAGTGATCCAGTTCGTGATCCGGCCGGTGGCGCCGCTGCGGCGGGGGCTNATNTACTTCGG
ACTNATTATCTCATCAAAGGACACCGGGCCGGTGGCTGGAATCCCATGGTGGCGATCGGCCACACAN
(SEQ ID NO. 512)

.....Rv376T7.seq:.....
CCGACCTGGTATCTTCCGATAGCGCGCTTGATATCCGGTCTGATCTCCTGCCCTTAACGCCGGATCTCAGCAGGTCC
CCATGCAAAGATCCGAGGTGTCCNGATCTAGGGGTCTCGTCTCCAGATGATGGAGCAAGTCGGCCC
(SEQ ID NO. 513)

Clone Rv377

.....Rv377SP6.seq:.....
CTCAAGCTTCGGCTCAGGCGCGCTGCCGGTAACGTGCGTGACCGGTGCAGGTTTCGACAATGTGGTGCCGGTTCGGC
GGCTACGTGCCATCAAGACACTGGCGCAGGCTATCGCACCCGTTATCGGCTACAAACAAATCGCGGTATGC
(SEQ ID NO. 514)

.....Rv377T7.seq:.....
CATCACCTGHTTCATGAACGGAAGCACCGCAGCGCTTCCTTTTCGGCCGCAACATGAGCCAGCCTCTCGTCGGCGGT
CGGGTGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCCTGAAACCAGCTTCCATATCCGCGACGAACGA
CGCCAGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCGTTCTCCACCGACCGGGCCCGGTGTGGG
GTGT (SEQ ID NO. 515)

Clone Rv378

.....Rv378SP6.seq:.....
AGCTTAGCTTCCCGCCCCGGCAATAGGGCTCCAGTCTATCCGGTGTGACCAGATAGGGGCCCAGGGTGATACCGCTGT
CTTTGCCCTTGGCCTGTCCGATGCGCAGCTGGCCCTCCAGCATCTGCAGTCCCGTGCGGACCAGTCGTTGAAAATGG
TATAGCCGATGATCGACCG (SEQ ID NO. 516)

.....Rv378T7.seq:.....
CCNGAACAGAAGCGGNGGTTCTACCGCGGTGTGCGGCCGGCGCGATATCGGCCTTTTACTAACCGAACCCGATGTG
GGCTCCGATCCGGCGCGCATGGCATCGACGGCGACGCCGATCGATGACCGCCAGGCTTACCACCTT
(SEQ ID NO. 517)

Clone Rv379

.....Rv379SP6.seq:.....
CTCAAGCTTGC CGGACTCGACAAGCATTCTTGACAGTTGTTTTGGCTCGGCATGGTTAGCCAAGGTTCTGCGGTCCCA
CCAGATCATCTTGGTCCGGTAGCGCTCGTCCGGGTATGCTGCCGCCGGGATTCTCGCTGCTATTACTCCCCCGAAGA
ACGCCACCGGTCCAGCGC (SEQ ID NO. 518)

.....Rv379T7.seq:.....
GCNAGGCGGTATAGCTTCCCGTGTACCGGCGACCGCCAGCCGAGAAGCTCGTTTTCCAGTGTTGCTGGGGATTCTC
ACGCTGCTGCTGAGTGCGTGCCAGACCGCTTCCGCTTCGGGTACAAACGAGCCGCGGGGCTACGATCGTGCGACGCTG
AAGTTGGTGTCTCCATGGACTTGGGGATGT (SEQ ID NO. 519)

Clone Rv37

.....Rv37SP6.seq:.....
GTGTGGAACCGTGAGCGGATAACAATTTACACAGGAAACAGCTNTGACCTTGATTACGCCAAGCTATTTAGGTGAGG
CTATATTAATACTCAAGATTGCGGTGCGACACATCGGCCCAAGAACCGCCGAAGGCACGGCGGAACGCCTGCGGCACA
TGGGGCGACGACGACGCGGTGCGACTTCTGGGCTGTCCAGCCGGATCGCGCCGTCGCGA (SEQ ID NO. 520)

.....Rv37T7.seq:.....
CACTGTCACTACATATGCGCCGCTCCTCCTCATCGCTGCGCTCGGCATCGTCGCCGGCGGTGATGGCGTCACCCTACC
CAAGCCGAACGCGAAGACGAGAACGTGTTCCATTATTAGGGTGTGAGCACCAATACCAGATTGCTCACCAGGAACCTCAC
GCAGCACCGGGACGGATGTGAGCCACACGCCCATCTGGGGTGGTAGCGGGGAAATACGGCTAACGCGGCTCCGGTGC
CGGCAGCCGACGCGAGACCTCGGCGGGCGGACACGGCAACACGACGACCCATAGTTGTTCTTTGCGGGATGGCCGT
GTTTGCGGACATATCGGGCGGGCGGCGGGCGCCGAGGTAGTGGCTGAGGCCCATCTCGTGCCCGCCGAATGGCC
CCAGCCAAACCGTGTA (SEQ ID NO. 521)

Clone Rv381

.....Rv381SP6.seq:.....
CTCAAGCTTTTACGGTGATCGCGCATCACCTGGTTCATGAACTGGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCAACA
TGAGCCANCCCTCTCGTCGGCGGTGCGGTGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCCTGAAACCAG
CTTCCATATCCC CGCAGACNAACGAC
(SEQ ID NO. 522)

.....Rv381T7.seq:.....
CTCAGAAGCCGCTAGCTGGTAGAGTCGCTGACCGGTGCACGTGGCGNCAATGTGCGCTGCCGGTTCGCG

(SEQ ID NO. 523)

Clone Rv382

.....Rv382SP6.seq:.....
CTCAAGCTTGCGCTCATCAAGCGGAACAGCAGGGCGGTGCGCTGGTGCCTATGACGGGTGACGGGACCAATGACGCA
CCC GCGCTCGCGCAAGCCGATGTCGGGGTGGCNATNAATACCGGCACCCAGGCGGGCCGGAAGCCGGCAACATGGTC
NATCTCCACTCC (SEQ ID NO. 524)

.....Rv382T7.seq:.....
ACTTCTATTTGACTGGTGTGCTGTGGCGGATCCGACTGCCGGCGTGGTCAAGGCCGGCCAGTTGTGGGATNCCACA
GGCAC
(SEQ ID NO. 525)

Clone Rv383

.....Rv383SP6.seq:.....
GCTTGTGCTATTCCGTGGCACTGTCAGACATATGCGCCGCTCCTCCTCATCGCTGCGCTCGGCATCGTCGCCGGCGGT
CATGGCGTCACCCTACCCAAGCCGAACGCGAAACGAGAAGCTGTTCCATTATTAGGGTGTGAGACCAATACCAGATT
GCTCACCAGGAACCTAC (SEQ ID NO. 526)

.....Rv383T7.seq:.....
CGATATTGCTCGGCCGCGTTGCTCTGACTGGGTGCGCT (SEQ ID NO. 527)

Clone Rv384

.....Rv384SP6.seq:.....
GACCTCGGCCACCAAGCCGACGCGACCGTTCGAGGTGGCGATCCGGCTTGGCGTCGACCCGCGTAAGGCAGACCACAT
GGTCCGCGGCACGGCCANCTGCCACACGGCACTGGTAAGACTGCCCGCGTCGCGCN (SEQ ID NO. 528)

.....Rv384T7.seq:.....
CCGGAAGTCTAGGGGACGACCTACTCAGCGCAAATGTCGCTAATGTGAGTCCGCCCCACCAGGGCAGATCAACCCAT
GTCGATGATGACCTACCCGGATACCGGATTGGCGGT (SEQ ID NO. 529)

Clone Rv385

.....Rv385SP6.seq:.....
AGCTTCAGTTCTCCACGACGCGTTCCCAAATGAATTTCCCGATCCCAATCTCGGTTGAGATACAGGTGCGCCATAC
CCCTTACTTTCGNAACGCTGGGCGGATTGGCCCTGCCGCTG (SEQ ID NO. 530)

.....Rv385T7.seq:.....
CCGCTACGGGTGCAACATGCATCCCGAGACCGATGCTCGAGCGCGCACCCCACTCGCCGATGGCCGGAACCGGCTGG
TTACCCGGGTGGCGGCTGACC (SEQ ID NO. 531)

Clone Rv386

.....Rv386SP6.seq:.....
GCGGCTGGTTACGACTCCCTGTTGTGATGGACCACTTCTACCAACTGCCCATGTTGGGGACGCCGACCAGCCGATG
CTGGAGGCCTACACGGCCCTTGGTGGCTGGCCACGGCGACCGAGCGGCTGCAACTGGGCGCNTTGGTNACCGGCAAT
ACCTACCGCAGCCCCGACCTGCTGGCAAAGATCATCACCACGCTCGACGTGGTTAGCGCCGGTCGAGCGATCCTCGGC
ATTGGAGCCGGTTGGTTTGAGCTGGAACACCGCCAGCTCGGCTTCGAGTTCGGCACTTTCAGTGACCGGTTTAN

(SEQ ID NO. 532)

.....Rv386T7.seq:.....
GCCTTTCCGCACAATCTGTACCCAGGACCNTCTAAAAAATCGAATACGACGGCGTGGCCGACTTTCCGCGGTACCCG
CTCAACTTTGTGTCGACCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAATACTTCACTGACGCCGGAA
CAAATTGAGCGAGCGGTTCCGCTGACCANTNNTGTCGGTCCCACGATGACCCAGTACTACATCATTGCGACGGAGAAC

CTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGAACCCACTGGCGAACCTGGTTCAACCAAACCTTGAAG
GTGATTGTAACTGG (SEQ ID NO. 533)

Clone Rv387

.....Rv387T7.seq.....
GCAGACCAACAAGATGCATCGGGATCATACGCCGTCAACTACCCGGCCAACGGTGATTTCTTGGCCGCCGCCAC
(SEQ ID NO. 534)

Clone Rv388

.....Rv388SP6.seq.....
CTCAAGCTTGCCAAAGAGACCTCGTCCACCAAGCNGGACGCGACCGTCNAGGTGGCGATCCGGCTTGGCGTCCACCCG
CGTAAGGCANACCANATGGTTCGCGGCACGGTCAACCTGCCACACGGCACTGGTAANACTGCCCCGCTCGCGGTATTC
GCGGTTGGTGAAAGGCCGATGCTGCCGTTGCCGCGGGGGCGGATGTTGTGGGAGTGACAATCTGATCGANAGGATT
CAGGGCGGCTGGCTGGAATTCGATGCCGCGATCGCGACACCGGATCAGATGGCCAAAGTCGGTCNCATCGCTCGGGTG
CTGGGTC (SEQ ID NO. 535)

.....Rv388T7.seq.....
CCACGGCGTGATCAAGGTACCGGCCGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGCTTGATGTGGCGTTAGCGC
CGGATTCACCACATCCCCTTGCAGAAAGTCGGTTGGGTGCAATGATGTAGCGCTTCTCCCATCGAGATAGTGGAGCA
ACGCAATCCGTGCGGTACGGTTCGGGTCNTACTCGATGTGCGCGACCTTGGCGTTGACACCATCTTTGTCAATTGCGGC
GAAAGTCGATCATCCGGTAAGCGCGCTTATGACCGCCGCTTTGTGCCGGGTGGTAATCCGGCCATGCGCGTTGCGTC
(SEQ ID NO. 536)

Clone Rv389

.....Rv389SP6.seq.....
GGCGGCTGCGTCGGCGAGATGATCGCCCGTGCCACCCCGATCCGTGCCTCGGTGAGCGCCAACGTGCTTCCGGTCC
GGCGACCACCATGTCGCATGCGCCGAC (SEQ ID NO. 537)

.....Rv389T7.seq.....
GCAATCGCCTTGGCGGTGCGCGGTTGTACCGGTGATCATCNGGNGCGGATGCTCATNCGGCGCATTTCTGCNAAT
CGTTCCCGTATGCCACCTTGACGATGTCTTCATATGGACCACGCCGATGGCCCNCGCGCTNCTG
(SEQ ID NO. 538)

Clone Rv38

.....Rv38SP6.seq.....
CCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAAG
CTATTTAGGTGACACTATAGAATACTCAAGCTTCCACATCGGTATGCCAAAGCATTGCGCCGCTATCGATTTGCGGCT
GGCATCGCAAGGTGGACTTCTTGCTCAGCGACGAGATCCCGTGGTCCGATCCGCGGCTGCGCGGGCTGCGACCCGTG
CATCTCGGCGGCACCCGTGACCAGATGGCGCGCGCCGAGGCAGACGTGCGCGCGGGACGCCACGCCGACTGGCCGATG
GTGCTGGCCGCGTGTCCGCACGTGCGCCGACCCGCGCCATCGACGAAACCGGCCGCGCTCGGTTCTGGACCTATGCC
CACGTGCCGTGCGGGTCCACGCTCGACGCGACCGAGACCGT (SEQ ID NO. 539)

.....Rv38T7.seq.....
CGCGTCCACCGCAGCGTGAGATTGGTGGCGCCATTTCGTGCTGGTGTAGCTGCTGTTGGCGGCGTCGCCGATTGTGCG
GGCCAGCCTTGTGCGGGGGCCGCTTCTACCCACGAGTCGGCACTTCCGCAACCGCCAGCTCGACCGCGATTACGGCG
GCCGAACGGCCGCCGGAAGGCGTCTCGCAAGCGCCTTATCCTTTCGAGGTTCCAGATCCTTCCGCTACGTGGGTC
GCTCATCGGCGGGCCCGGCCGAATGAGTACAGGTGAGGGTAACCGCTACAAATGAAGTTGGTCAGTGCTGGCCAACTG
TGTAATGGTTGCCCGGCTCGGGTACCACGTACATTCTGGCAAGGCGGGCGAGATTGGGTTCCGCGCTCCTTGGCCG
GTGGCGGTTCCCGGTTGTCCGTGGGCGTGTGCTGTACGTGGTGTAAAGTGTGCTGAACCTCCTCAGTTTGGGCT
(SEQ ID NO. 540)

Clone Rv390

.....Rv390SP6.seq.....
CTCAAGCTTGCGCTGGATCTGGCGGCTGAGCCTGTTCTTGGGCAACATGCCGAGGGATCGCCTTTTCCACCACGCGGT
CGGGGTGGCGTTGCATTAGCTCACCGATGGTGCGCTTGTGCAGGCCGCCGGGATACCCCGAGTGCCGGTAAACCATCT
TGTGCTGCAGTTTGTGCGCGCTGATGGCGACCTTGTGCGCGTTGATCACNATGACNAAGTACCGCCATCGACATTGG
GGGCAACGTGCGCTTGTGCTTGCCGCGCAGCAGGTTGGCCGCCGCGACGGCAAGGCGGCCAANACCACGTC
(SEQ ID NO. 541)

.....Rv390T7.seq:.....
TTTGGGATGGGCAAAAGGCGAAGCNCCGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGGCTAGGGCTTCTC
GCGGGAAGGCCCGAACGTACGGCGTTTCAACACGTGCGCTCGCCCTCCGACCGCGAACATTTCGGGGATGGCAGCAACC
TGGTAGCACCTGGCCGGGCGATGATCTGCAGCGTGCCTCGCGGGTAGTCGCCCGCCGGGCGGCTACAGTCTGAAACGC
GATGACCATCGATGTGTGGATGCAGCATCCGACGCAACGGTTCCTACACGGCGATATGTTCCGCTCGCTGCGCCGGTG
GACCGGTGGGTCTATCCCGGA (SEQ ID NO. 542)

Clone Rv391

.....Rv391SP6.seq:.....
CTCAAGCTTCGTCATAAGACCATGGTGCCTTTCTTTACCCGTCCANAGTCGGGGGCATCCGCACCGGCTCGCATCG
CATCATCTCCACGACGGGCGCTCATCGCTTGGGCCATTTCAATGTACTTGATACCCCGCGTGGGGTAGGCCA
CTGCNACAATTCAAACACGGTGTACACGGTGAATANTGTGNANATGGGCTCTGATCAACCGTCNCAAACCGGTTTC
(SEQ ID NO. 543)

.....Rv391T7.seq:.....
GAATTCTGCGTGACCGCTATGGGTTGCAGCAGCGGCTGGCGCCGCACACCCCACTGGCCCGGGTGTTCGCCCCGA
ACCCGGATCATGGTGAGCGAAAAGGAGATTTCGCTGTTTCGATGCTGGGATTGCCACCGCGAGGCCATCGACCGATTA
CTCGCCACCGGGGTGCGAGAGGTGCCGAGTCCCGCTCCGTGACGTCTCCGACGATCCATCCGGCTTCGCCCGTCCG
GTGGCGGTAGCCGTGATGAAATCGTGCCTGCCGCGCTACCAACAGGTGATTCTGTCCCGTTGTGTCGAAGTGCCTTTC
GCGATCGACTTTCGTTGACCTACCGGCTGGGGCGTCTGCACAACACCCCGGTGAGGTGCTTTTGTTCAGATTGGGC
GGAATCCGTGCTCTGGGTTACAGCCCCGAACCTCGTCNCGGCGGTGCGCGC (SEQ ID NO. 544)

Clone Rv392

.....Rv392SP6.seq:.....
GCAGTTGGGAATCGCTCTGCAGCAAACCANTATTCTGCGCGACGTTTCGAGAGGACTNNTTGAATGGACGGATCTACCT
GCCGCGCAGCAGCTGGACCGATTAGGCGTACNCTCCGCTGGACGACTCCGGGGCACTCGATGACCCCGACGGACG
GCTCGCGGCACTGCTGCGGTTTANTGCCNACCGCGCCGANACTGGTATTCGCTGGGACTGCGGCTGATTCCACACCT
CGACCGCCGCGAGCGCTGCCTGCTGTGCGGCCATGTCTGGCATCTACCGCGCTCNGCTCGCCTTGATCAGACCATCGCC
GGCGGTGCTCTACCATCGGCGAATCTCTGTTTCGGGACTGAANAANGCCCAAGTGGCGGCGGCGAGCACTGGNCTCTT
CGGTAACCTGCNGACCGCCCATTTGGACCGCTACCG (SEQ ID NO. 545)

.....Rv392T7.seq:.....
TTGATCTGGACGTCTGAGACGGTGATCGGNCCGAACCTGAATTGTCCGGTAATGCCAGCGCAGAAAGCANGGTGGTG
GCCGGGGCGGTGAANCCGGCGTCCGGCGGCACCGTCGAAGTCGATGTGGATTGCCGGAATGGGGATGTCCGGCACGGCG
AAGCCGTAGTTGCTTGTCCCGTGAGGCCANGTGGATGGGGGGAAGGATCGTGGTGTCCGGGATGATAATGGGGCCG
ATGCCGCGGTTGAAGTCCAGTGGATCGGGAATTCGGGAATCGTGATGCCGACGTTTCAGGCCGAACAGGCCCTCCAAG
TTGCCTCGCCACNAGATGCCGTTGCTGAAGTTGCCCGACATGAGGGCGCCGGTGTCCACATTGCCCGAATTGGCGACG
CCGGTGTGGC (SEQ ID NO. 546)

Clone Rv393

.....Rv393SP6.seq:.....
CACGTAGGCGCCGTCCATAAATNACTCCGCCGCGCTTCGCACATCCTCGTANCGATCCTTGGCGAGCAGGTCAACCGG
GCGCTGCCCGTCNAGGAGCCGGTTTTTGGCGTGACCCACTGGCCGACACCTCGGGGGGTAAAGCGAATCCGAGAGCAG
GAGGACNAGGTCACGAANCTGCGCCAGCCGGTCTGACCGCTCAGGGCGGATGTGCGCGGTCCGCCACCCCGGTACCGC
CCGATCGGACACCTGTATGACCGCGGCGACNTCGACCTGGGTGACGCCGAAGGTTTCAGGGCATCNACNATCTCGCT
GGCCTCGACCGCCCGGTCCAGGGTGACCGCCATCGTGTTTCTCCGCAACTTCGGGTTCTACTACCGTAAACGCTACC
G (SEQ ID NO. 547)

.....Rv393T7.seq:.....
CGGGGAACGGTCTCGCACACCTGGTTCTGTTGCGGGAATTACTCGGACANCAAAACGTCAAGAACTACGACGGCAG
TNGGACAGAAACGGCTCCCTGGTGGGCGCCCCGATCGAGTTGGGAAGCTGATATGTGCTCTGGACCAAGCAAGGAC
TGACATTGCCGGCCAGCGTCGACCTGGAAAAAGAAACGGTGATCACCGCCCGCGTAGTGGACGGTGACGGCCAGGCCG
TGGGCGGCGCGTTTCTGCGGCTGCTGGGACNCTCCGACGAGTTACCGCCGGGAGGTGCTGGCGTCCGGCCACCGGG
CGAATTTCCGGTTCTTCGCCGCGCCCCGGGATCCTGGGACCGCNGGCGCGCGCTGTT (SEQ ID NO. 548)

Clone Rv396

.....Rv396SP6.seq:.....
CTCAAGCTTTGTCCGACAAGCGTTCCCGGGCGGTCAGCAAGCGAACGTCCGGTTGGCCCACTGCGGGTTCGATATTGCCG
CCAGGGA (SEQ ID NO. 549)
.....Rv396T7.seq:.....

CGTCAGCACGGCGACGTCGCGNTACGCCGAGCAGTTACACAATCGCTCTGCAGCAAACCAATATTCTGCGCGACGTTG
GAGAGGACTTCTTGATTGGACTG

(SEQ ID NO. 550)

Clone Rv39

:::Rv39SP6.seq:::

CTGCATCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTAC
GCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTCGCGCAGCGGGCGGTTGACCCGGTTCACGCCGTCATAGC
TGGCCAATCTGGCATCGTCGATCANCATGTGGTGGGGGGTGACCTCGGCGGTGATCGAAATACCCTGGTCTTATCCC
ATTTACAGGATTTGACGGTGCCCGCGGCCGACGCGTGACAGATGTGACCCGGGCGCGCGCTACGGGGCCAGCAAGG
CGTCGCGGGCGACGATCGATTCTCGGCGGCCCGCGGCCATCCCGCCAGGCCCGCGCCCATGGGTCCCTCGT
GCGCGACGGCGCCGACCGTCAGCCGGGGCTCCTCGGCGTGCTGGGCGATCAGCACGCCCAAACCGGTG

(SEQ ID NO. 551)

:::Rv39T7.seq:::

CCGACGCGCACTACGTGCTGGTGTCCACCCGCGACCCGCGACCGGCGACGAGCTACGCAGCTACCGCATCGTCGATGGCG
CTGTACCGAGGAACCTGTCAATGTCTGCGAGCAGTACTGAACCGTTCGAGAAAGGCCAGCATGAACGTCACCGTAT
CCATTCGACCATCTGCGGCCCCACACCGCGGCCGAGAAGAGTGTCTCGGCCAGCGCGGATACCTTGGGTGCGGTCA
TCAGCGACCTGGAGGCCAGCTATTGCGGCATTTCGAGCGCCTGATGGACCCGCTTCCCCAGGTAAGTTGCACCGCT
TCGTGAACATCTACGTCAACGACGAAGACGTGCGGTTCTCGGCGGCTTGGCCACCGCGATCGCTGACGGTGACTCGG
TCACCATCTCCCCGCCGTGGCCGGTGGGTGAGCGGACACATGACAGGATACGACTCACTGTTGCATGCCTTG

(SEQ ID NO. 552)

Clone Rv3

:::Rv3SP6.seq:::

TGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG
CCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGCCGGGAGGGTGCATGGCCGACTCGGATTTACCCACCAAG
GGGCGCCAACGCGGTGTCCGCGCCGTGAGCTGAACGTTGCTGCCCGCTGGAGAACCTGGCGTGCTGCGCACCTG
GTCGGCGCCATCGGCACCTTCGAGGACCTGGATTTGACGCGCGTGGCCGACCTGAGGTGGCGGTGGACGANGTGTGC
ACCCGCTTGATTGCTCGGCTTGGCCGATGCCACCTGCGCCTGGTGGTTCGATCCGCGAAAAGACGAAGTTGTGGTG
GAGGCTTCTGCTGCCTGCACACCCACGACGTGGTGGCACGGGCAGCTTTAGCTGGCATTCT

(SEQ ID NO. 553)

:::Rv3T7.seq:::

GGAAACACCGNCGCCGTCGTGGCCACCAACACCGCGACACGACCGTGACCCGGACCGGGGTGCCGCGGAACCGGTC
TTGGCCAATTGCCGCGGCCAAGCCGTGCGCGCCATGGCGAACAGCACGCGGCATTGCCCGAGCATCAACACCATC
ACCACCGTGGTAAGCCCGGCCAGCGCGCCGACGAGATGATGCCGTGGCCAGTACACCCCGTTGGCCTGGAACGCG
GTGGCCAGATTTGCCGGCCCGCGCCCGGTACGGTCCGCAAGTTGGGTGTATGGAACCATGCCCGACAGCACACCGAT
ACCGCGACGTAGAGAAGGTACAGACCCCGAGCGACGCGAGAATCCCTCGAGGGACGCTCTCGTTGAGGACGCTTGGTC
TCCTCGGCCATGGTGGCCACGATGTCAAACCCGATAAACGCGAAGAACACGATCGATGCCCGGCCAGCACGCCGTA

(SEQ ID NO. 554)

Clone Rv40

:::Rv40SP6.seq:::

CCTGCTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTAC
CGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGTCTCGGGCGTGGCCTCGGCCAAGAAATCGTCGACGC
CGGCTCCTGTGCAATCGCCTTGGCGGTGCGCGGTTGTACCGGTGATCATCACGGTGCGGATGCTCATTCGGCGCA
TTTCGTGAAGCGTTCCCGTATGCCACCTTGACGATGTCTTCAGATGGACGACGCCGATGGCCCGCGCGCTGCTGT
TATCGGTCCATTCCGCAACGACTAGGGGTGTCCCCCGCGGAGCTGATGCCGTGCAATGGCACCCACCTCCTCAG
TGGGGTGGCCACCGTGATCGAAAACCACTTCATACCGCAGCCGCGGCACCTTGGCGATCCGAACGGATGCGCTC

(SEQ ID NO. 555)

:::Rv40T7.seq:::

TTCTGTCGATGGCGCGCCCGGCTACGGTTTGACCTGTGGGTGTGCAATTGGGGTCAAATTCGAGGTCGGCGCGCT
AAGAGTGGTCATCCTGCACCGCCCGGGGGCCGAAGTGCAGCGGCTCACACCGCGCAACACCGACCGAGCTGCTGTGCA
CGGCTGCCCTGGGTATCCCGCGCGCATGACGAGCAGCAGCAATTCGCCGAGCTGCTGGCTTCCCGGGTGGCGAAGT
GCTGTTGCTGTGCGACCTGTTGACTGAGGCACTACATCACAGCGGGGCGCCCGCATGCAGGGGATCGCCGCTGCCGT
CGACGCACCGCGGCTGGGACTGCCGCTGGCGCAAGAACTTTCGGCTACCTGCGTATCTCGACCCAAGCANGTTGGCG
CATGTGCTGACCGCGCATGACTTCAACGAACCTCCNTCCGACACGCCGAACGAAGTGTGTTGGTGTGCGTATGC

(SEQ ID NO. 556)

Clone Rv412

:::Rv412SP6.seq:::

GCGGCGAGTGTGGTGGGTGCCGAACACGAATCCAACGACGCACTGGCGGAGAGATACCACTTGCTGTACTGGAAGCAC
GTGCTGATGATCTCCCGTGAATGTGCTTGGCGCGCTCTATCGAAAACAGTGAGCATGCTGCG

(SEQ ID NO. 557)

.....Rv412T7.seq:.....
CAACCGCGCTCGGCGCGTCTGGGCTTCCGCCGGCTCCGCCGACAATTCTATCTCTGGATCAGCGGGGCTCTCCGGGC
CGGCCTCCGCGAACTCAACAGGCGCGCCTTCCGGCCGAAACATTCCCTAGCCATATATGATCGCACCTCGATACACG
ATCTGGCGGCAACACCGCAAAGCGTCCGACGGGCCAACCTCCGCAATTCAGGTATCCGGG (SEQ ID NO. 558)

Clone Rv413

.....Rv413SP6.seq:.....
GAAGGTCGGCGAAGGTGTGGCTGGNTGCCGATCACGAATCCAATGATGCAGTGGTCGGAAGATATTAGCCACTTGCTG
TTCTGGAGACAGGTGCTGATGATCTCCCGTGAATGTCCTCGACTCCGTCTATCGAAATCTGTGAACA
(SEQ ID NO. 559)

.....Rv413T7.seq:.....
TCCTGCGCTCTGGGCCATTCTCGGGTCTGCCGACAATTCTATCTCTGGATCTGTGGGGCTCTCTTGGCCGGCCTCNGC
GATCTCTTCANGGCGCGCCTTCCGGCCGAAACATTCCTATCCATATATGATCGCACCTCTATACACCGTTTGCGCGC
AACACCGCAAAGTGTCTGTCG (SEQ ID NO. 560)

Clone Rv414

.....Rv414SP6.seq:.....
AGCTTTACGCTGGCGTATCAGCGTTGGGGCCGCTGCCATTTCCGTCGCCCAACGCGTTGCCAGCTCCCTGCGCTGTCA
GGGCTTGCGCGCCAAACTGGCCACCGCAACAACTTGCTGAGCTTGATC (SEQ ID NO. 561)

.....Rv414T7.seq:.....
CTCTATCTGGCGTCACATTCGCAATCTTTAGATTGCAGATATCGATAAAATCACCCGCGCGACAAGACCGCCATGTCA
TCCTTTCGATGTTATTTGCCCGCCTGGGGAAAGCGCAACGACGTTGCCTACACGTTCCGCGCT (SEQ ID NO. 562)

Clone Rv415

.....Rv415SP6.seq:.....
AGCTTNCCTTGCATCTGCACCCGATCCACGTCAGCCACGTCGGCGTTCTCCACCAAGAAGTTGCGGGCATTCTCCT
TGCCCTGGCCGAGCTGCTCGCCCTCGTAGGTGAACCAGGCACCCGACTTGCAGGATGAGGCCCTGATCCACACCCATGT
CGATCAGCGAGCCCTCCCTGCTGATTCCCTTGCCGTAGAGGATGTGCAACTCGGCCTGCTTGAAGGGGGGCGAACAGT
TGTGCACGACAACCCCTTCGGCGACGAGGGTGTGCAGTTCTCGACCTCGAGGTCGAACGTTTCGTGCCGCCGCGGTTG
GCAGCACTTCTCGGATCACGGAATAGCGGANTTCTTCCGCCAGCATGTCTGTCAGGAATTTGTCTATCCAGGGCATCCG
CGAGCGCTGCACGCG (SEQ ID NO. 563)

.....Rv415T7.seq:.....
ACTGTCNAGGGAATGCTTCGCAGCATCTACCTGCAGTCGCTTGTGCATAAGCGGACGGCCCNACCTGTTCTGTGTTCCG
GGACACCAGACGCGGGAGCACCGGCAGTACGGCGAAAGGTTTGAGCGGAAGGAGTTGCGCAAATCGGGGCGCCCCAAC
ACCCGTCCGCAAGACGCGGTCAACGACCTGTTTCAGGCGATCAGGGTCACCGACTCACCTGCACTGAGAACAAGCGAT
CTGCTGATCTGCCAGAAGATGGACATGAATGTCCACGGCAAGCCTGATGGCCTGCCGCTCTTCCGGGAATGTTTGGC
(SEQ ID NO. 564)

Clone Rv416

.....Rv416SP6.seq:.....
TGAATTATGATCCCAGACAACTGCATCANTTTAGCCGCGTCGNATGCTATCCGCCGACGGTTTGGANCNGGTCCGT
GTCGTTTCGTGTTGATCTACCCGAAGTTGTGTCCGCCGCCGCCGGGATCTAGCGAACGTGGGATCGACAATCAGCGC
CGCCAACAAGGCGGACGCGGCTGCCACCACGCAGGTGCTGGCCGCGGGCGCCGATNAGGTGTCAGCGCGCATCGCGGC
GCTGTTTGGTATGTACGGCCTGNAATATCCGGCGATCAGTGCGCAAGTTGCCGCGTATCACCANCAGTCCGTGCAG
(SEQ ID NO. 565)

.....Rv416T7.seq:.....
AACGGGGACCNCAGAAACATTCAANAACGAGGGTTCGTACCAACGTCGAAACCGACGGTTGCCAGCCGGCCACG
ATATTGCTGCTCGAGGGTCCGCTGTACCCTCACCGAACGTGAGTCCCACACCGCGGAGCGGGCGACTCTGGCGTCCG
TTAGCAGCCGAGCTCAAGGTGTCCCGACCACTGTCTCGAATGCTTTTAACCGACCGGATCAGCTCTCCGCCGATCTA
CGTGAACGAGTGCTTGCCACGGCCAAGCGACTGGGCTATGCCGGACCGGATCCGGTGGCGCGATCGTTGCGGACCGCG
AAAGCCGGTGCGGT (SEQ ID NO. 566)

Clone Rv417

.....Rv417SP6.seq:.....
AGCTTTGGAGCCNCNCCGANCCNCCGGTACGCCCCGCCACCGCCGTACCCGGCACCAGCCCTTTGAGCCGTTCCGC
GTGGCCGCGGTGGANCTGGCCGACGAGGACTGATCGTGCTGGGCAAAGTGGTCGATGGCAGCTGGCCGCGGATCTG
AAGGTCGGCATGGAGATGGAGCTGACGACCATGCCGCTGTTCCGCGACNACGACGGTGTGCAGCGCATCGTCTACGCG
TGGCGGATCCCATCGCGCGCCGGCGACNATGCANAGCGCANCGATGCTGAGGAGCGGCGCCGATGAGGATGAGCGCGC
CGGAACCCGTTTACNTCCTGGGTGCCGTATGCACCCGTGGGGGAAATGGGGTAATGACTTC (SEQ ID NO. 567)

.....Rv417T7.seq:.....
TTCTCNCATCGTTCTACTNNGATGGGACGCTGCTGCCGAGGCGATCCTGGCCAACCGGCTCTCGCCGGCGCTGACC
TTGGCGGGGCGAACCTGAACCTTCTTCCGATGGGCGCTTGGGCCAAACGTACCGGGGCTATCTTCATTGGCGCTCAG
ACGAAAGATATTTCCGCTTACCGCTTCGTATTACGTGCTTACGCCGCGCAGCTGGTGAAAACCATGTCAACCTCACC
TGGTCGATCGAAGGGGGTTCGGACCAAGACGGGCAAGCTACGGCCACCGGTGTTGGGGATCCTGCGTTACATCACCAGT
GCGGTCGACGAAATCGACGGTCCCAGAGTGTATTGGTGCCGACCTCGATCGTGTACGAACAGCTGCACGAAGTGGAA
GCCATGACCACCGAAGCCTATGGCGCCGTGAA (SEQ ID NO. 568)

Clone Rv418

.....Rv418SP6.seq:.....
TTCTTCCGGGTACCGCTGATCGGCGGCACCATCACGCACCCGGTGCAGGGCGAGGCGGCCGCGGCTGTGGTGTTGCTA
CGGCCGGCCAGCCCGGTACCGGTGTGATCGCCGGTGGTGCGGCCGCGCGGTGCTGGAATGTGCGGGGGTGCACGAC
ATCTTGGCCAAAGTCGCTGGGCAAGTGAACGCGATCAATGTGGTGACGCCACCGTGGCCGCGCTCAAGCTGCTGCAC
CGTCCGGAGGAGGTGGCGGCGCGCGGCTTTGCCAATAGAAGACGTCCCCCGGCCGGGATGCTG (SEQ ID NO. 569)

.....Rv418T7.seq:.....
GTCGAAAGTGACCATCTCTACCTTGAGTGCCATACCGCCCCGACCCTATGCCTCGGATAGCTCGGCGGAAAGAAACGCT
TGCAGTGCCGCCGAATAGGCGGCTACGTGCTGAGCGCCCATCAACTCTCGCGCGGAGTGCATCGCCAGCTGGGCGGGC
CCGACGTCGACCGTGGGGATTCCGGTGCGCGCCGCGGCCAACGGCCCGATCGTGCACCCGACGGCAGATCGGCGCGA
TGTTCTGAACGCTGCATAGGCACTCCCGCGCGCTGGCAGGCCAGTTGCGAAACGCCCCCGCGGGTGCCTTCCGTCGG
TTGGCTTTACCGCAAATTTGGGGTTGCCCCT (SEQ ID NO. 570)

Clone Rv419

.....Rv419SP6.seq:.....
AAAGCCACGGAAACGATTGCCTACTGCCGAATCGGGGAACGGTCCTCGCACACCTGGTTCTGTGCGGGAATTACTC
GGACACCAAAACGTCAAGAACTACGACGGCAGTTGGACAGAATACGGCTCCCTGGTGGGCGCCCCGATCGAGTTGGGA
AACTGATATGTGCTCTGGACCAAGCAAGGACTGACATTGCCGGCCAGCGTCTACCTGGAAAAA (SEQ ID NO. 571)

.....Rv419T7.seq:.....
TTTCGCCACCGCNAGGTCGTGCGGTTCCAGAAAAGCGTGGTTTCGCCGGGCGCGAGGATTCGACGGTCCAACCTGACC
AGCCGGTCCCGCCACCCGTTAGGCAGGATCGCGGTGTCTATATGTTGCCCTCGGCATAAACGCCATTGCTGCGGTGA
AAATCGGACATCTCGCGGATTGCCACGTCTACATGATCCGCTTTGTCCCGCGCCGGGTCGTTGACAAACGCGATGTCTN
GCCTCCTGGGAAGCGGTGGC (SEQ ID NO. 572)

Clone Rv41

.....Rv41SP6.seq:.....
TCGCCAAGTGGATTCTGTCTCACCNACGAGATCCGTGGTCCGATCCGCNGCTGCGGGGGGCTGCGACCCTGCATCTCG
GCGGCACCCGTGACCAAATGGCGCGCGCCGAAGCAGACGTCTCGGCGGGACGCCACGCCGACTGGCCGATGGTGCTGG
CCGCGTGTCCGCNCGTNCNCCGACCCCGGCCGATCNACCAAACGGCCGCGCTCCGTTCTGGACCTATCCACGTGCC
NTCGGGGTCCACGCTCGACGCGACCGANAACTAACCAGCGTCCTCGANCGGTTGCCCCCGGCTTCCGTGACATCGT
GGTGGCGGGCGCGCCGT (SEQ ID NO. 573)

.....Rv41T7.seq:.....
GTACCGTCACCATGATCGCCCCATCGGCATCGGTGAGCTGATAGATCCAGCCGGTTTCGCCAACCCGGAGCGATC
TTGGCGCGCTGCTNGTNGTNCNCTGANACNTAGCCACCAACAGAGCCCGGTGTGCGACAAGANGACTGATCGGATCTCT
CCGGACACNTCGAGGGGGTNCNCTAGGAGNCCGGCGCCACCCGAGGTAAGCCTCCGCCAGCCTCACACCGCGACCG
GGTATCNCAAGTCGCGCAATAANCCACCACCTCCTCGGACCCACGTTGTATGCGGCTGGGT (SEQ ID NO. 574)

Clone Rv42

.....Rv42SP6.seq:.....
ATACTCAAGCTTAGACCTCACTGATGTGGCGGGACGCGGGAGATAACCGCGGTTTCAGCCGTTCAACAGTGGTGGTTC
CCACACCACTTGTGCTTTGCGAAGTAAAGCGATTGATTTGCTCGAAAAGAGGGCTGGCTGCTCGTGAGGGACAT
CCATGGCCGATACCTCAGCGATCTCAACGGTCAAGCGACTGCATGTTTGGCGCAAGGTATCGCTAAGCATAGGTTTCGT
GACGGATTGACAGCAAGAGCTTTCCAAAGATTGCTGTCCACATANTGATTGCTATCTCTACACCTCTTCGCCGGTGC
TGTCAGAGCCATTGCAATCAGTTATCTCGCTCGTGTGGAANAATTTCCAGCCTGCGTTGGACAAACCGCGTC
GCCAAAGCGGT (SEQ ID NO. 575)

.....Rv42T7.seq:.....
AGCTTCCCGAGAAACAGTGCATTCCCTAAGCAGCCCGTTGTACGCCGATGAGTGAAGAGTGCACGCAATCGCCGGAA
TCCGGCAAAGCCCTGCACAAGCGAAATCAACCCGAGGGCTGACAAGGCAACGTCGGTGATCCGTACCGCTGGTTGGA
CAAACGGCAGAAGGCGGCCTCGTCCGGTCCATCTACGCCGAGCACACTGGTGATAGCGCGCATCGGCATCGGTGCGGC
CACGGTGGAGACGACGTCGCGGGCGTCTGGGTGAGTAACCCGCCGACCAAGTTCTCGGGCAAGCTGGTGCACCATCGG
GCGCCACGTCCTCAACGCGCCACGCGCCATACCTGGTGCCAGTTGCTTGCGCATCCGGGTGTGCGCCGGCGGATCGGA
CGTCGAGAAACGCGAGCCACCCGTGAGAGTGACCCACGGCGCTGGACACGTGTCTGGTTAC (SEQ ID NO. 576)

Clone Rv43

.....Rv43SP6.seq:.....
CGGCCGGGATGTGCGCAATGGCAGGTTGTGCGCCGGCTTGATGTGCGCGTTAGCGCCGGATTCCACCACATCCCCTTG
CGAAAGTCCGTTGGGTGCAATGATGTANCGCTTCTCCCATCGAGATAGTGGAGCAACGCAATCCGTGCGGTACGGTT
CGGGTCGTATCGATGTGCGCGACCTTGGCGTTGACACCATCTTGTGTCATGGCGGCGAAAGTCGATCATCCGGTAAGC
GCGCTTATGACCGCCGCTTTGTGCCNGGTGGTAATCCGGCCATGCGCGTTGCGTCCACCGCGACCGTGCAGCGGGCG
CACCAGCGACNTCTCCGGGTTGACCGGTGATCTCGCGCAAATCAGATACGCTGGCGCCGCGACGACCGAGCGCTCGT
GGGCTTGACTTGCGAATTGCCATGGTCTAATCAGGTCTTCTCTCACCTCTCGTCGCCGGGCTAGGGCGCATGCGCT
GTCCT (SEQ ID NO. 577)

.....Rv43T7.seq:.....
TAGCGGTGTAACCAACTCCCGGTCACCACCCGCAAACCTCTGCGGCAACAGCACCGTCGACGCGTCAACCGGGCTG
CCCGGAATCCTGTGGATGGGCATCGAGTGCATGGTCACGACGTCCTCGGCGACCTAGTGGCGCCACCCGCGCGCTTGCCTCCCAT
GATGACACCACAAATGACGCGCCGACACCGGTGGGGACGGCCAGCACGAGAGCCGTGTGCGCGAAGTCGACGCTAATGC
CGTAGGCATTGGCCGTCAACAGGCGACGCCCCGCGTACCACCGAGTCCACGGNGGTTGGGCGGTCTCCTCGGCCAA
CCAGGCGTGAACCCGGCGGATCCGAATGCAGCAAGACCCGTGGGC (SEQ ID NO. 578)

Clone Rv44

.....Rv44-2ndSP6.seq:.....
CCATTGGTCGGTGTGCGCATACCANTACNACGCGCGGGGACCTGACGCGGCGGCGCAACCATTCGGTGGCCATCGC
CATCGTCTGCCACCCGGTCAACGGACGCACCTTCTCTGGCCGACCTAGTGGCGCCACCCGCGCGCTTGCCTCCCAT
CGATCCGCTCAACATGAGCAGCGCAAACCGGATACATGACATCTGCTGTGGAACCAAGTGACANATTCCGCCG
CCATGATGATCNTCGACCGTCCTCCGGATTGGTC (SEQ ID NO. 579)

.....Rv44-2ndT7.seq:.....
GCCGCGCTGGTCAAAGGGGCGTCCGAAGGANCCGGGCTGGGTAAACAAGTTCTGGCTCATATCCGCGAATGCGACGCC
ATTTGTGAGGTGGTGGGGTGTTCGTCGACGACNACGTGACTCATGTACCGGACGGGTGCGATCCCCAGTCCGACATT
GAGGTGCTGAGACCGAGCTGATCCTGGCAGATCTGCAACCCCTGGAGCGGGCCACGGGCCGGCTGGAGAANGAAGCN
CGACCAACAAGGCGCGCAAGCCGGTCTACGACCCGGC (SEQ ID NO. 580)

Clone Rv45

.....Rv45SP6.seq:.....
GATCCACTGACCACGATGACATATCGAAATGCTCGACGATTCCGATGGCGATCAAGGCCACGATGCCCTGGCGGTTGG
GCGGTATCTGGTGGATGGTGACCCGCGTAGGTTCCCGTGATCGTGTGACCCAGTCCACGCGATGGGCGGCGAGGT
CGTCGGCACGATACCCCCGCGTNTGCCGCCGAGTGCGCCTCGAGTTTGGCGGCCAGCTCTCCCCGGTAGAACTCTC
ACCGTTGGTCGCCGCGATCTTCTTANCGTCGCCGCGTGGTCAGGAAAGGTAACAGCTACCGGGTTTCGGCGCTCG
TCCGCCGGGATGAACGCATCTGCGAATCCGGGCTGGGATGCGAACAACGGACCTGTGCCG (SEQ ID NO. 581)

.....Rv45T7.seq:.....
TCTACTGCCGAATCGGGGAACGGTCTCGCCACCNGGTTGCTGTTGCCGAATTACTCAGGACACCGAAACGTCGAG
AACTACGAGCGGAGTTGGACANAATACCGCTCCNNGTGGGCGCCCCCATCGANTTGGGAAGCNGAAATGTGCTCTGG
ACCCACCCAAGAATGACATTGCCGGCGCCCTCAACTGGAAATAGAAACNGTGATCACCCGCGCGTCTTGAAG

GAATGGCATGCCCTGGGCCGGGCGTTCTTCCGCTGCCGGACTCCTCCCACCAATTCACCGCCGAAGGCGTCCCGTCT
GC (SEQ ID NO. 582)

Clone Rv46

.....Rv46SP6.seq:.....
ATACTCAAGCTTCTGTCAACGAAATCCCGCATGGGATAACGGGTTTAGATTTGACAACGGGACCGTGTCTCAACA
AGCCGGTCATCAGCTGGGCCGGCGACAACGGTATCTACTTCACCGCTTTCGCCCGT (SEQ ID NO. 583)

.....Rv46T7.seq:.....
CTGGCTCAAGCGCTCGGCCGCGCAGGTGAACCTCGGACCGGCTCGACGTCGCCGAACGCGAGGCGGTGCTGGCCACGCC
GACGCCGTCGTCGCACATATCGGCACCGTGCACAAGTCTACAACAACGCCGGCATCGCGTACAACGGCAACGTCGACA
AGTCGGAGTTCAAGGACATCGAGCGCATCATCGACGTCGACTTCTGGGCGTCTCCACGGGCCC (SEQ ID NO. 584)

Clone Rv47

.....Rv47SP6.seq:.....
CCGCCCTCCGCATTATGGGTCAAGAACCATCGGGTCGGACTTCTGGGCTTCCAACGCTCGCGCCGTCCCN
(SEQ ID NO. 585)
.....Rv47T7.seq:.....
CCGTGGCACTGTGACACATATGCGCCGCTCCTCTCATCGCTGCGCTCGGCATCGTCGCCGGCGGTGCTGGCGTCACC
CTACCCAAGCCGAACGCGAAACGAGAAGCTGTCCATTATTAGGGTGTGAGCACCAATACCAGATTGCTCACCAGGAA
CTCAGCGCAGCACCGGGACGGATGTCGGCCACCACGCCCATCTGGGGTGGTAGCGGGGAAATACCGCTAACCGCGGTCC
GGTGCCG (SEQ ID NO. 586)

Clone Rv48

.....Rv48SP6.seq:.....
TACTCAAGCTTGTCCAAATATCGAAGCGTCGGGTCGCGAGGCTCGGTCCGCGAGCTCCAGCAAAACCCGCTCCACCCCT
AGATGCCGGTATCCCTCAAGGTCTTTATCCGCCGCTTCACCCCACTGGCACACGGTCACCGGCACGTGCCCCCGGCC
ATGGCGCGCAACCGCTGAAGCGGACCCGACAGCCGCTGCGGTGATGGACTGATCGCGATCCACCCGGCATTGAGCCGG
GCTATCCGCGGGAAGTTCGCCGGTCCCCGCCCCACATACAGCGGAGGATAGGGCTTTGTACCGGCTTCGGCCAGCAG
TAGATCGGATCGAAGTCCACATATGTCCCATGGAATTCGCGCTGCTCCTGCGTTGAGATCTCGATTATCGCGCGCAAC
CGCTCATCGATCACACGTCCGCGCACCCGAGGGTCCACACCATGGTTGGCGACTTCTTCGCGCAACCAGCCACACCCA
CGCCGAAACGAAACCGTCCCTGCG (SEQ ID NO. 587)

.....Rv48T7.seq:.....
CAGGCATGCAAGCTTGGCCAACTCCTCATCGGACTTGAAGGTGCCGTCTCGTTGGCGGCCCTGCTCCACGGCACGTT
GATGGCACCAGGAATGTGTCCGGGCCGCTGGCTTTGTCTCGGCCAGGTGCGCGGGGGCCAGGATCTTGCCGGAGAA
CTCGTCGGGAGAGCGCACGTGATGAGGTTCTTGACGTTGATGGCCGCCAGGACCTCGTCGCGGAATGCCGAATCGT
GTTATCCGCGGGGGANGCGGTGTAGGAAGTCACCGGCCGGCTGACCGGTCGCTGGACAGCGGGCGTCCGTCGAGCTC
C (SEQ ID NO. 588)

Clone Rv49

.....Rv49SP6.seq:.....
ATACTCAAGCTTCAAAACAGGCCTGTTGTGGGCGCACCCGGCTCGCCGAGTTCTGCACGCACCGCCTCAAGTGCGGCC
CGCACCGCCGGCATCTCCGGTCACGCAGGGCCGCGGCCCGCGCCGACGACGGCGTGTTCGCGCAGTTCGCCGTCA
ATGATGCTGACCTGATCGGCCACCCGGGCGGTCTCGCGCTCGTCCGTTCACTAATCGCGGTGCTCAGCAGCGTCTCG
ACAGCCACACCCGAGTGGAGACCAGATGCNCCACCACGGACCGCAGCGATGCCAGTCACCTCACCGTCC
(SEQ ID NO. 589)

.....Rv49T7.seq:.....
CAGGCATGCAAGCTTTGCAAGTTGCTGAGTAATGTCGGCCAACGTCACCACAATCGCGATGAATTCATATGCCGCCC
AGGGCGGCCAACCAATGGTGGCCGCGAGCGGCAGCTCGATCGCAGCGCGGAGGTTGCCGGCCGCGAGTTGATTACG
AACAGGGTGAGGTATAGGCGGGCAGGATAGTGACGAAGGCAAGACCTAGATCTGCCGTGCGAAGAAGAATCGAGTAT
CCGGTCGACACAACGGAAGCGAAAGTGTCCGCGATGTTGATGAGCGTCGCCGGTGTGGCGGGCGGTGGCGGGGTAGC
ACCGTCCGCACATACCGCGGAACGCGGGCATCCGAATTTGGGGCAGGGTGTCAAGGCGGCTGGCAACTCACCATGA
ATCT (SEQ ID NO. 590)

Clone Rv4

.....Rv4SP6.seq:.....
CCGGCTCGTATGTTGTGTGGAATTGTGACCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAAG
CTATTTAGGTGACACTATAGAATACTCAAGCTTGGCCGCGAGGCCGAGTCGATTGGTCGCGGTCGCCTCGACAGTTAG
CTTATGCAATGCTAACTTCGGGGCAAAGTTCAGGCGGATCGGCCGATGGCGGGCGTAGGTGAAGGAGACAGCGGAGGC
GTGGAGCGTGATGACATTGGCATGGTGGCCGCTTCCCCCGTCGCGTCTCGGGTAAATGGCAAGGTAGACGCTGACGTC
GTCGGTCGATTTGCCACCTGCTGCCGTGCCCTGGGCATCGCGGTTTACCAGCGTAAACGTCGCGCGGACCTGGCTGCC
GCCCCGTCTGGTTTCGCCGCGCTGACCCGCGCTCGCCCATGACAGTGCGACCCCTGNACCGGGCTGGCC

(SEQ ID NO. 591)

.....Rv4T7.seq:.....
GTGTGCTGTCAATTCAGAGCTGAGCCTGATGCACTCAACTTACTGAGCATGCTAACGCTGGTCGTGCGGGTCTTGTTCC
CCGCGTGTGCGCAGGGCACACGCTCGGGGCGTAGCTGGGAGAGGCCCGGTCAAGCCCGGAGAGCAGTGCTCAGTCCG
CCAGCTTGACCGACTTTCGATGAGAACGCGCTTCTCGCCGTATTGAACTGGCGTGCTGACGGTCGCTGAGCAGCGCTC
GCCGAGTGCGGCCGCTGATTCTTTCATCGAGCCAGGAGGCGCATTCGTGTTGCGCCGCTGCGGGTCGCGCCCATCGT
CGACGCGATCCGTACCCACTCCTCGATCAGGTCTGCCTCATCGAACGGGCCAACGGTGCTGTGCGAGTAAAGTGTGCG
TGGGCACGCGAGCCGGTGCTGTGGTACACCCACCGTTGCATGAACAA

(SEQ ID NO. 592)

Clone Rv50

.....Rv50SP6.seq:.....
ATACTCAAGCTTCACCAGGCGCGGCGGGCGCGGCCAAGCCAGGCAGCCGCGCTCGGCGCGTCGGGGCCTTCCGC
CGGCTCGGCCGACAGTTGATCTCTGGATCGGCGGGGCTCTCCGGGCCGGCTCGGCGACCTCAGCGGGCCGCGCCTT
CCGGCCGAACCATTCCTAGCCATAGATAACCGCACCTCAATGCACGGTTTGGCGCAACCCGG

(SEQ ID NO. 593)

.....Rv50T7.seq:.....
AGCTTCCGTCACGACCCGCCCTCGCCGGTGCCGGCGCCATCGGTTCATCGGATCTCATGACGACGTCACGTAGGCCCGC
TAGCCGCGAGCGGGCGCGGTCAACTGGCGAGGCGGGCGGACGCTGACTGAGCTGGCCGAGCTGGACCGGTTACCGCG
GAACTACCGTTCTCGCTCGACGACTTTCAGCAGCGGGCTTGACGCGCGTGGAACGCGGCCACGGTGTTGCTGGTGTG
CGCGCCGACCGGCGCTGGCAAGACGGTGGTG

(SEQ ID NO. 594)

Clone Rv51

.....Rv51SP6.seq:.....
ATACTCAAGCTTGCCGGGACCGCGGAACAGAACCGGCGGTTCTACCGGGTGTCGGGCCGGCGGATATCGGCCTCC
CGACTAACCGAACCCGATGTGGGTCC

(SEQ ID NO. 595)

.....Rv51T7.seq:.....
ACGTTGGCTCTGCCGGAACGTATTTCCAGCGGCACGCATTCGGCGTGCGGGCGCCGAGTTGCGTCGCTGGGAT
CACGCAGCAGTCGCCGGCGGCTGCCGTGCGGGCTATGAATTGCACCGAGCCGGAATCCNCAC

(SEQ ID NO. 596)

Clone Rv52

.....Rv52SP6.seq:.....
ATACTCAAGCTTGTCGTATTCCGTGGCACTGTCAGACATATGCGCCGCTCCTCCTCATCGCTGCGCTCGGCATCGTCG
CCGGCGGTATGGCGTCACCTACCCAAGCCGAACGCGAAACGAGAACGTGTCCATTATTAGGGTGTGAGCACCAAT
ACCAGATTGCTCACCAGGAACACGCAGCACCGGGACGGATGTCAGCCACCACCCCATCTGGGGTGGTAGCGGGGA

(SEQ ID NO. 597)

.....Rv52T7.seq:.....
CGTTGGTAGCCGATATGCATAGTGTATCTTACTGAACATGATTTCCATTATGGAGCCCGGGGTGCCGGCAGCGCGAA
CGGTGCGCCGTCAGACGCGGGCGGCACTGACCAGGTGTTGCGGGCGAACATCGGCCCGGCTTCGGATTCCGGTCCGG
GTACCGGGCGACCCACCGCTTCGAGGTA

(SEQ ID NO. 598)

Clone Rv53

.....Rv53SP6.seq:.....
ATACTCAAGCTTGCCCAACTCCTCATCGGACTTGAAGGTGCCGTCTCGTTGGCGGCCCTGCTCCACGGCACGTTGAT
GGCACCAGGAATGTGTCCGGGCGCTGGCTTTGTTCCTGCGGCAGGTGCGCGGGGGCCATGATCTTGCCGGAACACTC
GTCGGGAGAGCGCACGTGATGAGGTTCTTGACGTTGATGGCCGCCAGGACCTCGTCGCGGAATGCCGAATCGTGT
ATCCGGCGGGGAGGCGGTGTATGAGGTACCGGCCGGCTGACCGGGTCGCTGGACAGCGGGCGCTCCGTCCAGCTCCCA
CTTCTGCGGGCGCGTCCAACNACTTGACTTCTCCTGG

(SEQ ID NO. 599)

.....Rv53T7.seq:.....

ATATCTTAAAGCGTCGGGTCCCGAGGCTCGGTCCGCGAGCTCCAGCAAAACCCGCTCCACCCCTAGATGCCGGTATCCCT
CAAGGTCTTTAGCCGCCGCTTCAACCCACTGGCACACGGTCACCGGCACGTCGCCCCCGGCCATGGCGCGCAACCGCT
GAAGCGGACCCGACAGCCGCTGCGGTGATGGACTGATCGCGATCCACCCGGCATTGAGCCGGGCTATCCGCGGGAAGT
TCGCCGGTCCCCCGCCACATACAGCGGAGGATAGGGCTTTGTACCGGCTTCGGCCAGCAGTAGATCGGATCGAAGT
CCACATATGTCCCATGGAATCCGCTGCTCCTGCGTCCAGATTCGATTATCGCGCGCAACCGCTCATCGATCACAC
GTCCGCGCACCGCAGGGTCCACACCATGGTTGGCGACTTCTTCGCGCA (SEQ ID NO. 600)

Clone Rv54

::::::::::Rv54SP6.seq::::::::::
ATACTCAAGCTTGTGCGGTAAACCCGCGAGGGCGGTGGGTGCGGTGTCAAAAACAACCACACTTCTTTGCGGTTC
GGTGATCTCGACACCGGCCGCGAGCCGACCATGCGCGCGTAAATCGGCGATCAGCGCGTCGGCTATCGCCTGGGT
GCCGCCACCGGAATCGGCCAGCCGACCGAATGGGCCAGCGTTGCCAGCATCAGTCCGGCGCCGCGCCGACACAGTGA
CGGCAACGGTGAAATCGGTGGGCGGCAACGCCGTGAACAACGCGCGGGCATCTCGCCGCCAGCGACCGCCAGGC
AGGGGTGCCCTGGGCCAGCATCCGCGAGCCCGAGACGCGAGGACCGAGCCAGTGCAGTAGGCAAAGACCGCTTGTGCGA
GACATGAACTCCACGACCGT (SEQ ID NO. 601)

::::::::::Rv54T7.seq::::::::::
AGCTTATTGAACCGCGGGTCCGAGGCAAAGTGGACCTCATAACGACTCGGGTCCAGCGACCGCGCCAACACGAACGGC
CGGACGAGCTGGGCCAGGGTCGCGGCCTCCCTACAAACAGGATCCGTTGCCTGCGAGCGACAGGCTCCGGTGCGGCG
TTGGGCGCCGTGCTCGTCCAGCGTCCGGTCCCGGTCGCCGCGCAGCTTGTTCCTCCATACTCGCCCCCTAATCT
CGAGGCAGCCCGTACCCGCGAGGCAACCTCCCAAAAATGCAATCCCCAAAATGCAATGCGTCGAGCTATTTCTCACAC
CGACCGCTAGTTGCGGATCAGAAATCCGTTGGGCGCGGAAGTCCAGCCGAATTTGTTCTCCGCTCCGCATCATGCTT
GTAATCGTTTGAAATTCATCCTCATATGCTCGATCGCTTCATAGGGTCCAGGCCAAACCGGGCA

(SEQ ID NO. 602)

Clone Rv55

::::::::::Rv55SP6.seq::::::::::
CTTCCGGCTCGTATGTTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCC
AAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGGCCACCTCCGCGTGTGTGGTGGAAACCATCTGAGCAGTGTG
CCAAACCGGGGCGAGACAGCTCCCAATTGACGTGAGCCGCTCACTTGCTGGGTAAAGCGTCG (SEQ ID NO. 603)

::::::::::Rv55T7.seq::::::::::
TAGCGCCCCCTCCCGGGCGGAGCTCCACGGCGTGGATCAAGGTACCGGCCGGGATGTTGCGCAATGGCAGGTTGTTGC
CCGGCTTGATGTGCGCGTTAGCGCCGGATTCCACCACATCCCCTTGCGAAAGTCCGTTGGGTGCAATGATGTAGCGCT
TCTCCCCATCGAGATAGTGGAGCAACGCAATCCGTGCGGTACGGTTCGGGTGCTACTCGATGTGCGCGACCTTGGCGT
TGACACCATCTTTGTCTTTCGCGGAAAGTCGATCATCCGGTAAGCGCGCTTATGACCGCCGCTTTGTGCCGGGTGG
TAATCCGGCCATGCGCGTTGCGTCCACCGCGACCGTGCAGCGGGCGCACCGAGCGACTTCTCCGGGTTGACCGGGTGA
TCTCGGCGAAATCAGATACGCTGGCGCCGCGACGACCAAGCGTCTGCGGCTTGTCTTGCGAATTGCATGTCTAATCA
GGTCTTTCTC (SEQ ID NO. 604)

Clone Rv56

::::::::::Rv56SP6.seq::::::::::
TGAACTATATAATACTCAAGCTTGCCAAAGAAGACCTCGTCGACCAAGCAGGACGCGACCGTCGAGGTGGCGATCCG
GCTTGGCGTCGACCCGCGTAAGGCAAACAGATGGTTCCGCGGCACGGTCAACCTGCCACACGGCACTGGTAAGACTGC
CCGCGTCGCGGTATTCGCGGTTGGTGAAAGGCCGATGCTGCCGTTGCCGCGGGGGCGGATGTTGTCGGGAGTGACGA
TCTGATCGAAAGGATTCAGGGCGGCTGGCTGGAATTCGATGCCGCGATCGCGACACCGGATCAGATGGCCAAAGTCGG
TCGCATCGCTCGGGTGTGGGTCCGCGCGGCTGATGCCCAACCCGAAACCGGACCGTCACCGCCGACGTCGCCAA
GGCCGTCGCGGACATCAAGGGCGGCAAGATCAACTTCCGGGTTGACAAAGCAGGCCAACCTGCCTTCTC

(SEQ ID NO. 605)

::::::::::Rv56T7.seq::::::::::
GCTGAGCTCCACGGCGTGGATCAAGGTACCGGCCGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGCTTGATGTGCGC
GTTAGCGCCGGATTCCACCACATCCCCTTGCGAAAGTCCGTTGGGTGCAATGATGTAGCGCTTCTCCCATCGAGATA
GTGGAGCAACGCAATCCGTGCGGTACGGTTCGGGTGCTACTCGATGTGCGCGACCTTGGCGTTGACACCATCTTGTC
ATTGCGGCGAAAGTCGATCATCCGGTAAGCGCGCTTATGACCGCCGCTTTGTGCCGGGTGGTAATCCGGCCATGCGC
GTTGCGTCCACCGCGACCGTGCAGCGGGCGCACCGAGCGACTTCTCCGGGTTGACCGGGTGATCTCGGCGAAATCAGA
TACGCTGGCGCCGCGACGACCGAGCGTCTGCGGCTTGTAATTGCGAATTGCCATGTCTAATCAGGTCTTCTCT

(SEQ ID NO. 606)

Clone Rv57

.....Rv57SP6.seq:.....
ATACTCAAGCTTGTTGGTGACCTCGCCGGCGAACAGTTCTCGCACGATTCCGGATTAGCGGGACTGGTCACCAAGTTG
GGTATGCGGGAAGGCGCTGACGTTCGCCGCGATTAGCTGTTTGATGGACGCGCGGTGATGTCCTGATCACGGAACTG
GCTGTAATAGCCCAGGGTCGCCACGCTTCCATCCGGGCCCGGACCCGGC (SEQ ID NO. 607)

.....Rv57T7.seq:.....
GATGATCGCCGGTGCCACCCCGATCCGTGCCTCGGTTCAGCGCGAACGTGCTTCCGGTCCGGCGACCACCATGTCGCA
CGCACCGACCAGGCCGAACCCGCGGCCCGCACATGCCCGTTGATGGCGCCGACCACCGGCAGCGGCGACTCGACGAT
GGCGCGCAACAGCGCGCTCATTTCCCGCGCCCGGCCACCGCCATCCGGTACGGATCACCACCACCTCCGCCGGCCCTC
GCTGAGGTCC (SEQ ID NO. 608)

Clone Rv58

.....Rv58SP6.seq:.....
ATACTCAAGCTTGCCGCAATCGAAACCAACCTGTTGTGCCGCAAGAAATTACGCCGTGGCCCGGCGCCGATCAAGAA
ACGCCCCGGCGCGCGCGGTGTCGTGATGGCATGACGGGCACCAATGTGCACGCCATTGTCGAGCAGGCACCGGTG
CCAGCCCCGAATCCGGTGACACAGGCGACACCCGCGCCACACCCGGTATCGACGGCGCGCTGCTGTTGCGCGCTGTCG
GCCAGCTCGCAGGACGCGCTGCGGCAAACCGCGCGCGGTGGCCGATTGGGTCT (SEQ ID NO. 609)

.....Rv58T7.seq:.....
TTGGCGGGTTGGCCACANCCCGCCGGTGACGGCGACGATGCTGGGCTGGTTGCGGCCCTGCGCCACCGCGGCTTG
CATGCTGGTTGGCTGCTTGGGACGATCCCGAAATAGTCCACGCGGATCTGGTGATTTTTCGGGGTACCCGCGATTAC
CCCGCGCGGCTCGACGAGTTTTCGCTGGACTACCCGCGTGGCCAATCTGCTGAACTCGCGGCCGGTGGTGGCCTGG
AATGTCCANCGCCGTTACCTACGTGACCTTGATGGGATCCGGGGGNT (SEQ ID NO. 610)

Clone Rv59

.....Rv59SP6.seq:.....
NCGTGGACACCGGTGTCGANCGCCACCAGCCGCATGTCTGCANGTCNATTCGGTCCTCGGCAACATCTTGAATGCCGA
GCAGCGCTGGGCGTGATCGGCAACCGGGGATGACCGCTCGCCGATCCGCTCGACAATCCCGGCGGCACGTGACATGC
CGGCGGACGGCTCGACGAGCTGGAACCTCAGCGACGACGATCCGGAATTGATCACCAGCAGGTGCTACTCATGGACC
CCTGCGCCTGAATCCCGTGATGGCCACGGTGTGACTATTCTGTCGACAGTGCAACCCGAGATAGTCTTACGGCTGCGT
(SEQ ID NO. 611)

.....Rv59T7.seq:.....
CATGTATTGCCGTGCTCACGGCGCCACGCTCGATGGTTTCTCGAAGTCTCCGGGCTGGTGTACAGCTTCTCGTTGATC
TCGTTGCCACGCGCTCCTCTCCCGCCGACGACCCGATCTCGATCTCCANAATGATCTTGGCGGCCCGCCGCGCTT
GAGCAGCTCCTGGGCGATGGCCAGGTTCTCATCGATGGGCACTGCCGACCGTCCACATGTGCGACGGAACAAAGATG
TCACCTTGCTCACGCGTGCCNAGATCNCANAAGGGCCGGACATACTGTCTNACTTGTCTTGGGCACTGGTCCGTGTC
AGCCACGTGACGGGTACTTGGCGCGATAACGTGGTG (SEQ ID NO. 612)

Clone Rv5

.....Rv5SP6.seq:.....
GCCACCACGACCCGGCCGTAACCTGCTCACGGAAATGCGGCCAGGCCGCGCGTAGCACGTGGTATCCGCCATAAAGG
TGACCTTAAGCACGGCGTCCCAATTCTCGAACGACATCTTGTGGAAGGTGCCGTGCGCGAAGATCCCGCGCTTGCTC
ACCACACCGTGCACGGCGCCGAATTCGTCAAGCGCGGTCTTGATGATGTTGCTGCGCCGTCTCGGTGGCGAOGCTG
TCCTTAGTTGGGACCGCCCGCCCCCTTGTGCGGAATCTCGGCGACGACCTCATCGGCCATCGCCGAACGGCGCCC
GTGCCGTGCGGGCGCCACCGAGGTCGTTGACCACGA (SEQ ID NO. 613)

.....Rv5T7.seq:.....
CAGGCATGCAACCTTTGTCCACACGGCGTCTACTCCGTGCAAGGTCCGACCGCTTCCACGTCCCGCCGTGACGGTGCT
CCATCTCCCTCAGCAACGCGTGAAAGTGGTCCGATCCCGCGGCTTCAGG (SEQ ID NO. 614)

Clone Rv60

.....Rv60SP6.seq:.....
GTTGAGACGCAACCAGCGACAACGACGATTTGGCGTAGCGGGCGGACGTCTGCTCGATTTCGATCACGTGCGCTCGCA
TCGAGCATGGCCCGCGACGCTACACGATCGCCGTGCTGATGACACGACCGAGCCGTACGCCGGCGGTAAGCCGCGCC
AGGATTGCGCGAAAAACGTCTACGTGGCGGGTGTACTGGGTGTGCAATGATTCTGTTGGGTGCGTATGCGTCTTCAAT
CGTCGACATAGATCCGTGCGCGCATCGGTCGACAACTCCGGGTGAGTGGAAATACACTTGCCGATCACCGACGTGCG

CGGATCGATGCCGACCGAAATACGACCACATGGCTCTTGTGTCNCAGTGTGGCGGCATCAAATACCCTCAGTGCCGT
CCGAC (SEQ ID NO. 615)

.....Rv60T7.seq.....
TTNCCGCCTTNACGCCTACTCCNAGACGATGCTCGACGCGTGTGAGCACACGGCGCTGCTGTAGACGGCACGGCGCAG
CTGGATCGCGCTTGGTGCACCAAGCCTCTACGCGCGTGCCTGCGTCATCGGGTACCGAACATATTCCGGTCTGT
GCGCAGAGTGTGCATGTGCGGCTCTTGTGAACGAACATAGCAAAGCGTATATGTCTGTGGCGGCTCTGCAGATATCGC
GATAATACGTATATACATAAGGTGGCGCGCATCTATCGGTATATCCGTTATGGCGGACGTGCGTGAGCGTGAGTCGC
GGCGCATCGCGCACTTCGCGATCGCGTGAATGCTCCTCGCGACTGCGCGCATGCGTAGC (SEQ ID NO. 616)

Clone Rv61

.....Rv61SP6.seq.....
GGTGATGACGCACTTGTTCGAATGAGTCATTGACTACTCCCGTGGTTGTCTGCGATGGTGGAGTGCCGCGCAGCCT
TGCCCCGANGTCGCGATCGCGTGCAGGGCTTCGGGGAGCAGACTGACCTGCAGATGGAAGTCGTGCCACATGCCCGCGA
ACGGCGAGCTCGATGCTTGTTCGAAGNGCGCANGCGGTTTCGATCTTGTCCGCGTCAACGCAGATCGGATCTCGCC
GCGGTCTGCATGACGATGGCGCGCAGGCCCGCTCATGTCCCGTAGACGGGGAGATACGGGCGAGCCGCGGATCGAGACCT
ACGTAGCGCGGCGCCCATCGTGCCATCGACGAAGAATGACGGATCGCGCAGCGCCGTGCGTCTCGATGTACGC
GAGATCGCCACGGCAGATCAGCGATGCGCGGGC (SEQ ID NO. 617)

.....Rv61T7.seq.....
CGGTACGCCGGCAACAACGCCTTGTGACGAGCGCGTCCGAGCGGTTCATCGGCCCTCCACCGTCATGCACAGCTCCTTC
TCCAGGTCTACGCCGACGTGCGGGTCCACATTTGGTGAGCTTGGCGAATGCCTCGGCAACCTCGTCGAAATGCGCCTCC
GCGTCCGCATCGAAGGTGCGCCATGTCAAAGATCAACTCGACGTAGTAGCTAGTTACCGCATCAGGTCACTGTTTGTCTG
GCCTCGGAGTCCGGCCGAACAATGGCCATTTCCCGGACTCTAGAATCCAGTCATCGTCTCGGTGACGACGCCTTGCC
GATCACATAGCTCGACCGGATCGGAGAGAATCTGGTTCTCGT (SEQ ID NO. 618)

Clone Rv62

.....Rv62SP6.seq.....
ATACTCAAGCTTAAGCGCAGCAGTACCGGCGGTGCCTGGGCATCCAGCAAAACGGGGAGCTCAACGAACGATTCTTG
AACGAAGGGTCGTCCACCAACCTCAAACCGAACGGTTGCCAGCCCCGGC (SEQ ID NO. 619)

.....Rv62T7.seq.....
GCAAGTCCGCTCAATGTGGTTGTGATCACANGACTACGTGCGCTCAATCAGCTCAAACGTCAACCCCGTGGCGTGCTGC
GCAGATGAAGGTGCGCGCGCCGACGATGTGGCGGAAGCAACAGGTAATAACTGGTTCGGCATGGGTCAACCCCTCATTG
GGCCGTTGCGGATCGGGTGCACGCCCGGAGTGCCGGTCAACTCAACACCGCCTTACCGATCTTTTCGTGCAAAATG
GCGGTCTGTGCGGGTATACGTCCGCGATCCACGAGGCGGAATCCGCTGAGCCGCACTGA (SEQ ID NO. 620)

Clone Rv63

.....Rv63SP6.seq.....
ATACTCAAGCTTCCGCGCCCTCAAGCGGCTGAAGGTGGTTCCGGCGTNCCAACNGTCGGGCAACTCGCCGATGGGCATG
GTGCTCGACNCCGTCCCGGTGATCCCGCCGGAGCTGCGCCCGATGGTGCAGCTCGACGGCGGCGGTTCCGCNCGTCC
GACTTGAACGACCTGTACCGCAGGGTGTCAACCGCNACNNCNNGTGAAGGCTGATCGATCTGGGTGCGCCGGAA
ATCATCGTCAACAACNAGAACGGATGCTGCNGGAATCCGTGGACGCGCTGTTCGACAATGGCCGCGCGGCGGCGCC
GTCACCGGGCGGGCAACCGTCCGCTCAAGTCGCTTCCGATCTGCTCA (SEQ ID NO. 621)

.....Rv63T7.seq.....
TGCGCATGGCAGTTGTTGCCGGCTTGTGTCGCTTAGCGCGGATTCCACCACATCCCTTGGGAAGTCGTGGGTGCAAT
GATGTAGCGCTTCTCCATCGAGATAGTGGAGCAACGAATCCGTGCGTACGTTGGGTCTGACTCGAGTGCAGCANTT
GGCGTTGACACCATCTTTGTATTGCGGCGAAGTCGATCATCCGGTAAGCGCGCTTATCGACGCCGCTCTGTGCCGG
GTGGTAATCCGGCCATGCGCTTGCCTCCACCGCGACGTGCAGCGGGCGCACACCGACTTCTCCGGGTGACGGGTGATC
TCGGCGAATCAGAACCTGGCGCGGACACAGCGTCGTGGCTGTACTTGC (SEQ ID NO. 622)

Clone Rv64

.....Rv64SP6.seq.....
TGGGTGATCAGATACTGGCTAGTTGGTGGGTGGGGTGTGATCGAAGATCGCGGTGGCCGGCAGCGTTACTGCGGTGACG
CTGTTAAGCGGTTACGTACTCCACGGCACTCAANGAATTANATCCCGAATCGGCAAAACCTGGCCAGCGTCGAGTCCG
CAGCGCGCTGCGGCCCCACCGCTGCGGCATGCTCACATACCACCTCGATCGCTGCGGGAGTTGCTCGTGGCGCGAC
CGACCGGCCAGCGGGCGGCAACCGGAGGACCAAGATTACGACACCACCATCGCTAGCCCGATCTGGCGGCGGCGG
(SEQ ID NO. 623)

:::Rv64T7.seq:::

TCGTAGCGGTTGCGACCANTCCGCGGACAGCTCCGCCACGCGACGGGTCTGGGATCACCGCGGTCAAACCACCGAGCGG
CGAGGATCTCTGGCCGTCGACGTGACCGCGCACGCGCGGTGATGGCCAGTCCCAGACCGCGTTCCACTTGGCGTAC
GCGCTGGATGTGTTGTGCCGCAACGGAATCCACCTCAATTATGACCTCGTTGTGGGCGAGCGCGGTATCGTACGCCC
GACCAGGAATCGTCGATGCTATCTCACGTACCGAAGGCTCTCCAGCACACCGCATCCAGAACGTGCACACNGTCG
ACATGTCTCGGCGGATCCGCCTGCAGAACGAACGCCANGTGCGCTGTGCGACACGGGTCTGGCATCACCGCTCGCACGC
GGAGATCGGCACACGCGCAGCGCATCGATCATAATCTCTCGATGCGGTCTCCACCACCGAACAG

(SEQ ID NO. 624)

Clone Rv65

:::Rv65SP6.seq:::

ATACTCAAGCTTCGCTGAGGTGGTGGGGCACGATCACGTACCGCACCGCTGTGGTGGCGCTGGATGCCGGCCGGAT
CAACCACGCGTACCTGTTCTCTGGGCGCGTGGCTGCGGAAAGACGTCTGTCAGCGCGTATCCTGGCNCGGTCTGTTGAA
CTGTGCGCAGGGCCCTACCGCAACCCGTGCGGGGTCTGCGAATCCTGCGTTTCGTTGGCGCCCAACGCCCCCGGCAG
CATCGACGTGGTAGAGCTGGATGCCGCCAGCCACGCGGCGTGGACGACACCCCGAGCTGCGGGACCGCGCGTTCTA
TGCGCCGCTCCACTCACGCTACCGGTACCGGGTATTTATCGTCGACGAGGCGCACATGGT

(SEQ ID NO. 625)

:::Rv65T7.seq:::

GCACCTACGCTGGTACAAGACCTTCACAAAATCTGAAATCCTGACCCGATACTTGAACCTGGTCTCGTTCTGGCAATAA
CTCGTTCCGGCTGCAGGACGCGGCGCAAACGTACTTCGGCATCAACGCGTCCGACCTGAATTGGCAGCAAGCGGCGCT
GCTGGCCGGCATGGTGCAATCGACGACGCTCAACCCGTACACCAACCCCGACGGCGCGTGGCCCCGGCGGAACGT
GGTCTCGACACCATGATCGAGAACCTTCCCGGGGAGGCGGAGGCGTTGCGTGCCGCCAAGGCCGATCCGCTGGGGT
ACTGCCGACGCCAATGAGTTGCCGCGCGGTGCATCGCGCGCGGCGACCG

(SEQ ID NO. 626)

Clone Rv66

:::Rv66SP6.seq:::

ATACTCAAGCTTGATATAAAAAGATCGGTGAGCGCATCGATTGCTCCGCCGGGTTTGCCGCTGCGGCGCGGAGCTGC
CGTGACCGTCTATTTGGGTGATCAGATACTGGGCTAGTTCCGTGCGGGTGGGGTGATCGAAGATCGCGGTGGCCGCA
GCGTTACTGCGGTGACGGCTGTTAAGCGGTTACGTACCTCCACGGCACTCAAGGAATTAATCCCGAATCGGCAACG
CCTGGCCAGCGTCGAATCCGGCAGCGCGTCCGCGCCAGCACCGCTGCGGCATGCTCACATACCACCTCCATCGCTG
CGGCGAATTGCTCGTGGCCGACCGACCGGCCAGCGGGCGGCAAACCCGGAAGA

(SEQ ID NO. 627)

:::Rv66T7.seq:::

CCTCATCATATGCCGATAGAGCTCTACATATTCAGGAGATCACCATGGCTCGTGCGGTCTGGGATCGACTCGGGACCAC
CAACTCCGTCGTCTCGGTTCTGGAANGTGGCGACCNNGTCTGTCGTCGCCAACTCCGGAGGGCTCCAGGACCACCCGTC
AATTGTCTCGGTTCGCCCGCAACGGTGAGGTGCTGGTCNGCCAGCCCCGCAAGAACAGGCAGTGACCAACGTCGATCGC
ACCGTGCGCTCGGTCAAGCGACCATGGGCAGCGACTGGTCCATAGAGATTGACGCAAGAAATACACGCCCGGAGATCT
CGCCGCAATTCTGATGAACGACGACCCGAGGCTACTCGGTGANGACATNACGACGCTTATCACACCCCGCCTNC
TTCAATGACCCACGTCNGGCACCAAGGACCCGGAATCGCGGCTCACTTGNGCGATNGTCNACAACCAACGCGNCGC
CTGGCTACGGGCTCAACAAGGCANAAGACACAATCCGCTCTCGATTGGTG

(SEQ ID NO. 628)

Clone Rv67

:::Rv67SP6.seq:::

ATACTCAAGCTTATCGAGGCGGCGCATACCGAAGCGTGGGAAATCCAGACCGAATACCGCGACGTGCTGGACACTTTG
GCCGGCGAGCTGCTGGAAAAGGAGACCCTGCACCGACCCGAGCTGGAAAGCATCTTCGCTGACGTGAAAAGCGGCCG
CGGCTCACCATGTTTCGACAACCTCGGTGGCCGGATCCCGTCGGACAAACCGCCCATCAAGACACCCGGCGAGTCGCG
ATCGAACGCGCGGAACCTTGCCCCAGCCGCTCCCGAGCCGGCGTTCAAGGCGGCGATTGCGCATGCTACCCAAGCC
GCTGAGGCCCGCCCGTCCGACCCGGCCAAACCGGGCACGGCGCAACGGTTGCGCCGCGCGCACCAACCGGTCCGGTGA
CCGAGTACGGTCCCCCAGCCTGACTACCGTGCCCGGGCGGCT

(SEQ ID NO. 629)

:::Rv67T7.seq:::

TGGCCGGGCTGGTAGCCCGCGTATGGCAAGGTTCCGCTCAATGTGGTTGTGATGCAGCAGGACTACGTTTCGCTCAAT
CAGTCAAACGTCACCCCGTGGCGTGTGCGCAGCATGAAGGTGCGCGCCCGCACGATGTGGCGAAGGCAACAGGT
AAGAACCTGGTGGCATGGGTGAGCCCTCATTGGGCGTTGCGGATCGGGTTGCAGCGCGCCGAGTGCCGGTCGAA
CTCAACACCGCCTTACCAGATCTTTTCGTCGAAAATGGCGTCGTGTCCGGGTATACGTCCGCGATTCCACAGAGGCG
GAATCCGCTGAGCCGAGCTGATCCGGGCTCGCCGCGGCGTATCCTGGCCTGTGGTGGTTTCGAGCATAACGAGCAG
ATGCGAAT

(SEQ ID NO. 630)

Clone Rv68

.....Rv68SP6.seq:.....
GTCCAGTCAAGCATCGGTCTCTCCGACTACGCCAAGANTGGCGACGTGTCACTGCANACAGCGGANATGGTGGCGCC
TATGCGTCGACGCTCACAAACNGCGGTGANCGCGTTCTGGTCGTGCACCATCGAGCCGTGCCAGCCCGGCCGCGTGCC
GTCAGCCGCATCCACTGGATGCCTTCTCGGNGTTTCAATCANGTACANGCGACGTTCCGCCACCATCGTGCCGGGGCAC
GGTTAGCGAGAAACCGCCGACTTCACCGATTGCCTCGGTGATGCCGTGGAACAGATCGGGCCTATTGTGCGACAGCCAG
TGTGATNCGTATTTGCCGCCGTGCTCCTCGTCGCAACGATGCGAACACAGATCCGTGGNGGACGATAGCGGCTGACAA
NGTGGGGGCAACACAATCACATGCCACATTTCTTCATTTACGCCCACAACCCAGACTTCGTCTCGATGNGCCG

(SEQ ID NO. 631)

.....Rv68T7.seq:.....
CACGCGGTCTGGCCCCGATCCGAAGATCCCTTTGCCGGCGTGGCGGCTCTGCTCGGCGGTGTTGTACACTTCTCGAACA
CCTCGGCACCGACACCACCACCGTNGCTTGAACACCGCCAACATCGGCAGCAGATCTTGATGGTCTCTGGTGAATCCCA
CGGTGACTTTGGAGTGGAAGGCCCATACTGATCGCCGCCCGCCAGCACATGAGCTAGCGGCAGGAAAACCAGCAGCCGC
TCACCTTGCGCAGCAGCGTCNGGTGATATGCCTGGCGCCCTTAATCTCGTGAACCAAGTTGGATTGGGTCAACTGGCAG
CCTTGGGTCTCCGGTGGTGCCGANGTGTANATAAGTCCCGGGTCCGTCAACGTANTGCGCAGGCGGCGGTTACTCGG
CGGGTCAACGAGCCCCGCTCGTGAGCNATCAGCCTTTGGACCGAACGGGATTCATACTCCGCAGGCGGCCCTCCGAAA
TCGGCACATGTCCTTTGATCGTTCGCAACAN (SEQ ID NO. 632)

Clone Rv69

.....Rv69T7D3.seq:.....
GGCCATGTACATCGGTGGTACAGGTAAACCGCGCCGTGTGCGCGGTCTCGGAGATCAGAACGTGGTGCAGTTGAAC
CGCGGGCTTTAGCCAGTCGCGATAATCGGCGGAAGTCGGCGCCTGCCGCCCCAAGTACGCGGACTCGCCACCTAGCA
CACCGATGGCGAAGGCCATGNTCCGGCCACGCCGCCGCGGTGCATCACCAGTCATCGACTAGGAAGCTAAGCGACA
NCTTGTGCAGGTGTTCCGGGAGTAGCTGCTCGGAAAATCGGCTGGAACCGCATCAATGGTCCGTTCAATCGAACCG
GTTACCCGATCGTCAAAAAATCTCCGTCCT (SEQ ID NO. 633)

Clone Rv6

.....Rv6SP6.seq:.....
GGGTCTACAACCACCGGGTCTGACTTCTGGGCTTCCACCGCTCGCGCCGTGCGGACAAACAGCGCGGTGGAACCGACA
CTCGTTGTGATGTCCAGCTATCACCTCCGGTAGGCACCCAATCGACCCTACCCGGCTATCTCACCCCGATCTCCAG
GCTCCGCGGATCCATGCGCATCCCGGTCCGGATCCC (SEQ ID NO. 634)

.....Rv6T7.seq:.....
CAGGCATGCAAGCTTGTCTGATTTCCGTGGCACTGTGAGACATATGCGCCGCTCCTCCTCATCGCTGCGCTCGGCATCG
TCGCCGGCGGTGATGGCGTCACCTACCCAAGCCGAACGCGAAACGAGAACGTGTTCCATTATTAGGGTGTGAGCACC
AATACCAGATTGCTCACCAGGAATCAGCGCAGCACCAGGACGGATGTGAGCCACCACGCCCATCTGGGGTGGTAGCGG
GGAATACGGCTAACGCGGCTCCGGTGCCGGCAGCCAGCGCAGACCCTCGGCGGGGACACGGCTAACAAACGACGAC
CCATAGTTGTTCTTTGCCGATGGCCGTGTTTGCTGACATATCGGGCGCGGCGCCGGCGCCG

(SEQ ID NO. 635)

Clone Rv70

.....Rv70SP6D2.seq:.....
NCTACGCTGCTGAATGTTGTGCGCCGGAGGANTCAAGACCCACGCGGTTGTACGCGGACNTGGGACATGTTCAACCG
CCGGA (SEQ ID NO. 636)

.....Rv70T7D3.seq:.....
CTAACCAACAAGCCATGGTGGTTGGCGCCGTGAGAGGTGCGCGGTGCGCACAAACGGGAAGATCGCCTTGAGCGTCGC
TCGACCGCCGCTCGAGTTGGGTGATAACGAAGTACTGATGCCGATCATGTGACGCTGTCCTGCGCATCAGCGTGCAG
CGGCGACCCCTCGACGAGCCTCGGTGCCGCCGCGGCCAGGGCACCAGCTGTTTTAGCGCATTGTGCTCCGCCCGGTAAT
AAAGGANGTCGGTTCGCTCCGCTGCTGTGGTTGCGGAATAACATCTTCCCTTCCTGCAACAGGATGAGAATGGTTTAA
ATTGCTC (SEQ ID NO. 637)

Clone Rv71

.....Rv71SP6.seq:.....
CTAAGCTTTCCGGTCCGCCGCCACTAGTACCGCGTTGCCGGCCCCGCCGACCTAGAATGTTCCGCCCATTGCCGTTTC
CTCCCCCGCGCGGTT (SEQ ID NO. 638)

.....Rv71T7.seq:.....
TCTGGTGCCGGGTGTGCCGACGGGTCCGTCCGCCTCTGCTTCAGTGATTCTGTGATGCGACCGGCAACGTCCTCGTTG
TTCGGTGTCTATGTGGTCCGTCTCTCCTTGTTCGCATACGATT (SEQ ID NO. 639)

Clone Rv72

.....Rv72SP6D2.seq:.....
GCGATCGNTNACCACAAGGGCGCAACCGTTGCGCGCTCGACTGAACGTGCTGCGGCCTGGAGAACTGGCGCTGCTGCC
ACCTGGTCGGCGCATCGGCACCTTCGAGGACTGGATTTGACGCGTGGCCCCGACCTGANGTNGCGGTGGACNNGTGTG
CACCCGGTTGATTCTCGGCCTTGCCGGGATGCCACCTGCGCCTGGTGGTCGAT (SEQ ID NO. 640)

.....Rv72T7D3.seq:.....
CGTGACCGGACGGGGTGCCGCGCAACCGGTCTTGCCCAATTGCCGGGGACTGGGGCTGGAGTATAAAGCGGGCCTGT
TGCCGGAAGATAAAGTCAAAGCGGTGACCGAGCTGAATCAACATGCGCCGCTGGCGATGGTCGGTGACGGTATTAAACG
ACCGCCAGCGATGAAAGCTGCCGCCATCGGGATTGCAATGGGTAGCGGCACAGACTGGCGCTGGAAACCGCCGACGCA
CATTAAACCATAACCACCTGCGCGGCTGGTGCAAATGATTGAAGTGGCACGNCCTACGCGCAATATCCGCCAGAACA
TCACTATTGCGCTGGG (SEQ ID NO. 641)

Clone Rv73

.....Rv73SP6.seq:.....
ATACTCAAGCTTCTTACCCANAGCATGAACCCCGCCGTCCAATGCCGCCACCGTGGTGTGTCGGCCGGCCGGGTGCG
GGCACAATCGCCGAGTTCGGCGAACAGATCCTCGAAGGTCTTCACGGCCAGCGATTGTTGCACGTGTGAGCCAGCCAA
GTCACGGTGGTTTGACGCCACACGTTCCGCCACCGCCGCGCCGCGCATTAGGGCATCCTAATATAGGTTAGGCTACCCCT
ANTTATTCTGTGGTCAAGGAGGCGAGCCGAACGTGACCTTCCCGATGTGGTTCGCGAGTTCCGCGCGGAAGTGCCGTCA
GCATGGCTGTCCACCGGCATGGGCCCCGGTCCGCTGCTGGCCGCGGCCAGGGCGTGGCACGCGCTGGCCGCGCAATAC
ACCGAAATTGCAACGGAACCTCGCAAGCGTGTCTCGTGCAGGCAACTCGTGGCAGGGGCCCAGCGCCGACGGTT
CGTCNTCCCCATCAACCGTTCCGTATTGGCTAACACCTGCACGGTGGCACCGCACAAACGCCGCCACAAACGCGCCCC
GGTATAC (SEQ ID NO. 642)

.....Rv73T7.seq:.....
GGCCGAACCTAATCGGTTGTTGGCGGCTGCCGAGTTGGGTCACTCGGGGGGTGTGCACTGGCACATGGTGGGCCGGAT
TCAACGCAACAAAGCCGGTTCGCTGGCTCGCTGGGCGCACACCGCTCACTCGGTGGACAGCTCGCGGTTGGTGACCGC
GCTGGATCGGGCGGTTGTTGCGGCGCTGGCCGAACACCGTCGTGGCGAGCGGCTCGGGGTTACGTCCAGGTGAGCCT
CGACGGTGACGGATCCCGGGGCGGCTCGACAGCACGACGCCCGGCGCCGTAGACCGGATTTGCGCGCAGGTGCAGGA
GTCAGAGGGCCTCGAACTGGTCGGGTTGATGGGCATTCCGCCGCTGGATTGGGACCGGACGAAGCCTTTGACCGGCTG
CAATCGGAGCACAAACGGGTGCGTGCGATGTTCCCGCACGCGATCGGTCTGTGCGGGCATGTCCAACAACCTTGAAT
CCCGTCAACATGGTCGAC (SEQ ID NO. 643)

Clone Rv74

.....Rv74SP6.seq:.....
GTTTCCCTGATACTCGACCAGCCCCACTCGGGCCAATACGTGAATGTCCTAGCATTTTTACCCGTTACGGGCTAG
TCGAGTAGTAGACGATTGATTAGCCTGAACGTACCTCCGACGGCCAGCTGACGAACGGGTTTGACGGA
(SEQ ID NO. 644)

.....Rv74T7D3.seq:.....
TCAGCTGTCTGTAGAAGGGCTGGCGATACTGTGCACTGTCTGATATCGCNCNCGTNGTGGGACTATNCAGNCCATNANG
ATGCGGTTTCNNGNNNTGCAGAGNATCCTGGNACACATNCGGTTACGTTAATCANCATCGCGANTTNTNCGTNTTCG
ATTANTTCTGCTAACGNNCTCTNNAGTGCCTGCGGGTCGACTCTAGAG (SEQ ID NO. 645)

Clone Rv75

.....Rv75SP6D2.seq:.....
NCTCTGCCGGGNCAGAGCGCAGAGTCGGACGGCTTCGTGATCGTGAAGCGACCNTGCGATGANAGATATCGNTNAC
ACTGCTCANAAACTTCGGATCATCGNTGATACACAGGCCAACGGGTAGCGGTTGTCCAACCGCTTCGTCAACGANATG
GGATCGTGACGANCTACGCTCGCAGGATATGTCGCNGACCNGNTCTAGANAN (SEQ ID NO. 646)

.....Rv75T7D3.seq:.....
CACTTCATGCTCGTGCGTTGGCNTCGATTTGCNCGAGNGGTTAGCTCCTCGAGTGNGTGACGTATCACTCCGGCNGAC
TANCCGTATCNGCGTCCCGCACCGGTCACTGGTCTAGCCACACGGGGAGAAATNCNCGACCGGNGCTATCGACCNAT
CACGGCTGTGCGNNAAGATAGNCAGCC (SEQ ID NO. 647)

Clone Rv76

.....Rv76SP6.seq:.....
ATACTCAAGCTTGCCAACCGCCACCCTGCATCCGGGGGGCGAGCACTGCTCCGCCGACCAGTACGAACCAACCTGCGG
TGCCCAGGCCATTGACAAATGTGCTGGTCGGCGCCCGCAGTTCTAGCACAGCAACGCCGCGGCCACACAGGGGCG

(SEQ ID NO. 648)

.....Rv76T7.seq:.....
CGGTCCGTGTGCTTGGCGGCGTCGGTATCAACACCGCCACGAAATGGGGCACAAGAAGGATTTCGTGGAGCGGTGGC
TGTCCAAGATCACCTCGCCAGACCTGCTACGGGCACTTCTACATCGAGCACAACCGTGGCCATCAGTCCGGGTGT
CCACACCGGAAGACCCGGCGTCGGCGCGGTTTCGGCAAACTTTGTGGGATTTCCCGCCCCCCC (SEQ ID NO. 649)

Clone Rv77

.....Rv77SP6.seq:.....
AATACTCAAGCTTCGCGGAGGTGGTGGGGCAGGAGCACGTACCCGCGCCGCTGTCCGTGGCGCTGGATGCCGGCCGGA
TCAACCACGCGTACCTGTTCTCTGGGCGCGTGGCTGCGGAAAGACGTCGTACGCGCGTATCCTGGCGCGGTGCTTGA
ACTGTGCGCAGGGCCCTACCGCAACCGTGGGGGTCTGCGAATCCTGCGTTTCGTTGGCGCCCAACGCCCCCGGCA
GCATCGACGTGGTAGAGCTGGATGCCGCCAGCCACGGCGCGTGGAGCAACCCCGCGAGCTGCGGGACCGCC

(SEQ ID NO. 650)

.....Rv77T7.seq:.....
GATGGCACTCACGCTGGACAAGACCTTCACAAATCTGAAATCCTGACCCGATACTTGAACCTGGTCTCGTTCCGGCAA
TAACTCGTTCCGGCGTGCAGGACGCGGCGCAAACGTACTTCGGCATCAACGCGTCCGACCTGAAATTGGCAGCAAACCG
GCGCTGCTGGGCCGGGCATGGTGCAATCCGAACAAGCACGCTCAACCCGTACACCAACCCGAAGGGCCGCTGGCCCC
CGGGAACCTTGTCTCCA (SEQ ID NO. 651)

Clone Rv78

.....Rv78SP6.seq:.....
AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTCTGGGCGTCGTGGTGCCC
GGCTGCCGGTGCAGGAAGTGGATTTTACTGCCATCTCTCGCGACCCCTGAGGTGGTCCAGGCTTACAACACCGACCCA
CTCGTGACACACGACGGGTTCGGGCCGGGATTGGCCGCGCGTGTGCANGTGGGCGAGACCATGCCGCGCGGANCA
CCGGCATTGACCGCGCCGCTGCTAGTGTGCACGGCACCGATGACCGGCTGATCCCCATCGAAGGCAGCCGTGCGCTG
GTCNAATGTNTNGGATCNGCCGACGTGCANCTGAANGANTATCCCCGGCTGTNCCACNAGGTGTTCAACGAACCGGAN
CGCAACCAAGTG (SEQ ID NO. 652)

.....Rv78T7.seq:.....
CAAGGCATACGCCAAGACCCAGGGATCGCAGTCACCTCCGTCAACGGCCTGGTCCGCCGGCCACGGGTCCGTGCAGGA
GACGTGGCTGGCCATGCAAAGCGCCGCCCTTATCAGGAACGCCCCGGCTGTCCGGCTTTTCTGCATCGACACATT
TCCGGAGGTGTTGTGGTTGGCGCANCGCGAGACAGGCCTGGGATGGCGTGCATCGTTCATCGGGAATGCGATGGC
AACACTGAACTACGAGCGCATCTGCGCCAGCATGACTGTTTCGACTACGTCGTGCTTGGCGACGGGGANGTAGCGTT
CACCAAGCTGGCCTTGGCCCTGGCGAATGACCTGCGGTTGACGACTCCCGGGACTAACCCGCCGTANTGAGCAAGGAC
AGATTCTGCGCACACCCTCTCGCTGGTCGACCTTGACA (SEQ ID NO. 653)

Clone Rv79

.....Rv79SP6.seq:.....
AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGCCGGTGATCTGGGTGGC
CAACTCGGCGGGCACCATCTCCATCAGACNGCAAACGCTCGGGCTTCGGCGACAGCGATCGCGTCTGCGATNGTTTG
TTCGGCGGCGCTCTCCGCGGCCCTGCACCCGGAAGCCGCCCAAGGTGTTGACNCTTTGCGGGGTGAAGCCGATGTGTGC
CATCACCGGGATNCCCGCCGCGTCCAGACANGCGATTGCTCGGCCACCCGCTCACCGCCCTCGANCTTGACNGCATG
TGCGCCGCCGCTCCTTGAAGAAACCGGTGGCGGNGGCAACCC (SEQ ID NO. 654)

.....Rv79T7.seq:.....
CGTTGAGATCCAGCTGCGCACTGTGCAGCGCCTCGGTGGTCTGCTCGGCCCTGCCGGGATAACTCGTTGAGCTTGCCCA
GCGCGTCGTCCGCCGATCAGCCAGCACATTGCGCGCCAGGACGCCGGAGGAGACGGTGAAGCTCGAAAGAAACCTA
TGGCGGACCGCATGATTACACGCGCGATCAACCACCTCTGGTCGAGCCTCAAAATTTGCTTCTTAAACGGGCCATCG
ACGGATGACGTCGAGCTGGTTAGGTCTCAAACAGGTTACGAAACGATCTCGGAATTGTCCAAAAGGGGAAGTTAAGA
AAATGGATAGATTTCTACCATTTCTGCTGTGGACGATCGTACTTCTGCTATAGGGCTCCAGGGGCATCGACACGCAACG
ACCTTACGCGACACCGGATCCGCGCTGGCGGCGGAACGGCACANGCGCAACCGAAGGGCCAATCCGACATCGG

(SEQ ID NO. 655)

.....Rv263T7.seq:.....
CGTAATCACGATCCCGCTGAGACACTTGACCTTACGGCCGAAGTGACTTCGCTGCTGCTATGCCGACACCCGATTTC
ATACGCTGCTGTACACGACGGCCGGCCGGTGGCTCCATCACGCTCAACCGCCCGAACAGCTCAACACCATCGTCC
CGCCCATGCCGACGAGATCGAGGCCGCTATCGGGTTGGTGAACGCGACCAGGACATCAAGGTCATCNTNCTGCGCG
GTGGCGGGCGCGCCTTCTCCGGCGG (SEQ ID NO. 297)

Clone Rv264

.....Rv264SP6.seq:.....
CAAGCTTAAGCTGGTTCGGGCCACTCCATGAGCCGTAGTGCAATGGTTCGTGCACGGCGAGGCCGAACCTGCCATAAA
CATCCCTGACGAAAGTCTCCGGCAAGCCGATTGCTTCTTCGGGCCGCTTCTTGTGGATTGTCCGATAACCCGGTCCCT
CATGCTGGAAGTTGTGCGCACTCTTTCCTTCCGCGATGTGGGCTAACGACTCGTCATTGAGCAAGAAGTACGTGCACA
GGCATCGTCCGCCGGGCTTCAGCACGCGGGAGATCTCGTCCAGATAGTGCTCCAGTCCGGNGGGAACATGTGGGTG
AACACCGAGGTNAGAAACACNCATCCAACGACGCATCCGGGATATGAAAGCGAAA (SEQ ID NO. 298)

.....Rv264T7.seq:.....
TATGGTCTTCGTGACCACTACGTGCTAGGCGCCATGAGCCAGCGACTGAAGCCGCGCCATGCCTGCACGGCCCGCTC
ATCCAGCGAGGCGGCCATCTCCCGCAGATAGCCTGCCGCTCGGCGCGCACGCTGTCCGGATCGCGTCCGAGCTCGTC
GGCCAGCGCACGCGCGCTCGTCATACCATCGGGCATCCAGCAGTTGGGTAACTCAACGGGGTTCGGTTCGCTAGCGG
CGTCATTGATTAGCAACAATACCGATGCGCTGCAGCAACTTTCGAGTCCGATGCGGCCCACCTCCCGTGCAGTCAC
TGGCTAGCCCCCGTCATGCCGTTGTGTGATGGCACGGCAGCGGGTCTGTAACCTGCGGTCTCAGTTCGCTGG
(SEQ ID NO. 299)

Clone Rv265

.....Rv265SP6.seq:.....
GCTTAGCGGTCTTGCTCGAACCAGATTGCGTGCCACTCATGAGCGGTGGCGGTTCGCGGTGCTTACACATCT
(SEQ ID NO. 300)
.....Rv265T7.seq:.....
GTATCTGGCGCTCTCGAATATCCTTGACGTCCCGGGTGCCACCCAGATAGATCGCAGCGCCCTGCAATGGAGTTC
CCTTTATGGCCTCTCTAGCCTCCCGCTTGATCGGCTCGACCCGAGAGATGCCCTCGGGCGTTGCGGGATCTCCCTCCA
(SEQ ID NO. 301)

Clone Rv266

.....Rv266SP6.seq:.....
CTTCACGCCGATCCGCGACCGCGAACGCGACGGTGACGGTGGGCGACAAGGTTTCGGTTGGTTCGCCGCGCGCTGGGCG
ATATCAGCTCACCCGGTTTCGAGGTGTTTCGGCGACCGGACGGTGCTGCAGACATTCTTGAGCGTCTCGACCGGCCCG
ATTTCGGCTTCAACATCGTGACGCCGTATTTTCGGCGGTACCGCTCGGCGCCGAGTCAAGGCGGCCCTGAGCTAAAGCC
GGGCAATTGGCGGAGTGGTAAACAAGTTCGGTGACTTCGGTTGACCGACTCGACGGGCTCGATCTGGGCGCGCTGGACC
GGTATCTGCGTTTCGTTGGGGATCGGGCCNACCGCNANTTGCGTTGCGANCTGATTCCGGTGGAGCTCCAATCTGACTT
CCGG (SEQ ID NO. 302)

.....Rv266T7.seq:.....
GCAGCTACCGACCTAGCGACGAGTGTGTTTCGCAGCGTCAATGTGAACGTTTCGGCGTGATTTCGGCGCGCGGGTTCCC
GCTCTCAGCGCACGTTTCGGCGCGGAGNGGCTAGTCCCTGGTTAAGCAATGTCTCGGTTCGCCGCCAGCAGCGCGCATG
TCGCCAACCCTCNACCGGTTGCGCATGTCCGGTACCGACGGAACGACGGCGCGATCCGGATGTTCTTGTGTCGTCG
GATCCTTTTCGATACGGGAACGACCCCCCGCTCGGTACCGCGATACCAACGTCCTTAGCCAANGCTACNGTCCGGCG
CGCGGTCCCGGGAACACGTCGAAGCTGATGAANTAACCACCTTGGGCTCGGTCCAAGANGCGATCTTGGACTCCTT
AACCGCTGATNCAA (SEQ ID NO. 303)

Clone Rv267

.....Rv267IS1081N60.seq:.....
TCCCCATCGGCGCCGACCGTTTGAAAGTCCAAGCACGGGTGGGATGGAATCGACGACAGTTGAGCGCGCTCGGTGGC
CGTGGTCAGCAGCTGTTTCGCGAACGCACAGGTACATCCCTTCGACATCTCACCGACGTGGCACGGGCGACATCAAC
AGGAAGATTGACGAATCCCTCGCAGGCGCGGCACGTCCGACGGCCAACGCCAACTACGGGGCCACAGCGATCCTCCG
CTCACGCACCGCCAAAGCCAGGCTCANCCACCCAAGTCGGCCCCGCGCTCTCCCTCGCCCCCTGGTCTCCGGGGCCTT
GTTAAACAACCTACCGGAAGTCCACCAATCCTCGCTGCATCTCGACACCGTCCGCTCACTCCCTTCTCCCGCCCCCTC
TCCACACNACACCTCTTGATTAAGTACGCGAGCGGTCACTTTTCGTGCGACGAAATTCGCAATCCGGCCGCTCG
CCGCCAGAGAT (SEQ ID NO. 304)

.....Rv267SP6.seq:.....

CGGAAAGTGGATACTCCCAGCAGGTAGCAGGTCGCCACCACGCTGGTCAGTGCGCGTTTACGCTCGCTTGCGGCGCTGC
AGCAGCCAGTCCGGGAAATAGCTGCCCTGGCGCAGCTTGGGGATCGCGACGTGATGGTTGCGGCACGGGTGTCGCAA
ATCACGGTGGCGGTAGCCGTTGCGCTGATTGGACCGCTCATCGCTGCGTTGCGGCTAGCCCCGCCCGCACAGGGCGTC
GGCTTCAGCCCCCATCAAGGCGCGA (SEQ ID NO. 305)

::::::::::Rv267T7.seq::::::::::
GGCCGAGTCCAGCACTTCGCACTATGTGCAGACCAANACCCGGTGGTCGCCGCGCTGCGGCAGCGGCTGGCAACGGC
GCCGGTGATCACCGAGTGGTGCNAGTTGCCGACCGGCAGTTTCCCGCGGGCTTACTACGAGAAGGGCTGCGCGACG
TCATCAGGTATCACGTGTCGATGACGTCGAGCGTTAACTTCCCCGACCAGACGGCGACCTCGCCGATGGACCCCGCT
TGTAACCTGGTGTGGGCGCAAGCTAACGCCGCCGANGCTATCGGTACTCGGTGCGAAGCGCAGCCGGGGTCGCAAGCGC
TAGCGGGCAAGGTCGCGACGATCTCGGTACCTGGACCAACTACGGCGCTGCTGCCGCCACCGAATAGTNGTGCCCG
GCTACCGGCTGGTGGATTCCACGGGACATGTGGTTCGGACCTGCCGGCAGCGGTGGAAGTGAAGANGCTGGTCT

(SEQ ID NO. 306)

Clone Rv268

::::::::::Rv268SP6.seq::::::::::
AGCTTCAAGGACATCGTCATCGCAGACAAAACCGGAGCTAGGTGCGCATCCGGGAAGCATCGCGACACCGTGGCGCC
GAGCGCCGCTGCCGGCAGGCCGATTAGCGGGCAGATTAGCCCGCCGCGGTCCCGGCTCCGATTACGGCGCCCGAA
TGGCGTCACCGGCTGGTAACCACGCTTGC CGCGCTTGGCGGGCGGCTGCCGGATCAGGTGGTATATGCCGACAAAGCC
TGCCTGATCGGTATCACCAACGGTGACAGCAGCGGTTGTGCACCATCGCNAACGCCACCCCGGTCTCCGGGTCTGT
CAN (SEQ ID NO. 307)

::::::::::Rv268T7.seq::::::::::
GCTCGCGGTCCAGCAGCAGACGTGTCTGACCCGACGCCCCGGCCGCGGTACCGAAACCGGATCGGCCCGCCGATGGC
CGCGGCCACGGCGTCTGCCCTTACCCGGCCCGGATACAGCAGCCACACCTCGCGGGAACGCTGAATCGCCGGCAGGGT
CAAGGTGATTCGGCGTGGCGGCGGTTTCGCGAATCGTCCACCGCCACCACCATGCGGGTGTCTCGAAGACGCGGGGC
TGTGCGGGAACAGCGAGTTAATGTGGCCCTCGGGCCCCATGCCAGCAGGTGGACGTGGAATTGCGGCCGGGTACCC
TGGTGCGGCACTGGCGGCC (SEQ ID NO. 308)

Clone Rv269

::::::::::Rv269SP6.seq::::::::::
AGCTTGTGATCGTCCGGCAGCGTCCGGCGAGTCAAGTCAAGCCAGTCCGGTCTCCTCTCCGACTACGGCCAAGAAC
TGGGCGACGGTGTGATGCATACAGCGGANACTGGTGGCGCCCTAGGCGAGCGACCGCTCACAAACGGCGGTGACC
GCGTCTGTGTCGTGCACCATCGAGCCGTGCCATCCCGGCCGCGTGCCGTGAGCCGCATCCACTGGATGCCCTTCTCG
CGGTTTCAATCAGGTACAGGCGACGTTGCCANCATCGTGCCGGGGCANGG (SEQ ID NO. 309)

::::::::::Rv269T7.seq::::::::::
TTGGTGATCATCGNCCCAACGACCCGAGGCGATGTTCTTGACACCCGAGGAGTGTGCGAAGCTGGGGCTGGCCTTCG
CCGCCGATCCGTCTCAGCAGCTGGCGAAGCTGTGCGGGTGAGGAAATTGCGAGGCTCGTCAACGGTGTCTTACTTG
TTACCAACGACTACTAATGGGATCTGCTGCTGTCCAAGACCGGCTGGTCAGANGCCGATGTGATGGCGCAGATCGAC
CTGCGGGTGACCACATTGGGTCTAAGGGTGTGATTTGGTAGAACCTGACGCACCACCATCCAGCTCGGCGTTGGTC
CCCGAAACAGCCAGACCGA (SEQ ID NO. 310)

Clone Rv26

::::::::::Rv26SP6.seq::::::::::
GGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAAGCT
ATTTAGGTGACACTATAGAATACTCAAGCTTGATTTTGATCATCATGATGATCATCACCCGAAGTGTGGTAGCCGCGAG
TGGTTATCGTGGGTACCGTCTGCTTTCCATGGGCGCCTTTTCGGGCTTTCCGTATTGGTCTGGCAGGACATTCTGG
GTATCGAGTTGTACTGGATGGTGTGGCGATGTGCGGTGATCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGC
TGATTTCCCGGTTGAAAGAGGAAATTGGGGCCGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGGAG
TGGTGACGGCTGCCGGCATGGTGTTCGCCGTTACCATGTGCTTGTGTTGAGCGATTGCGAATT

(SEQ ID NO. 311)

::::::::::Rv26T7.seq::::::::::
CAGGCATGCAAGCTTGGCGTGCCGTTCCAACCCGAATTGGCTTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTC
AACGACGAGCTCGTCCGCGGGACACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTA
CAACGCCGCGCGGAACGCTTCCGCCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTGCATGAC
GGCATCGCCACCGGAGCGACGGCCAAGGCGGCGTGCCAGTGNCCCCGGGCGCACG (SEQ ID NO. 312)

Clone Rv270

.....Rv270SP6.seq:.....
GGCATCTTGGCCGCCATGTTAGCCACACTGCCACCGGTATAGAAGCGATGCGCACCGTCCTGCCAGCACATTGCGGC
GCTCCTCCCTGGAAAGCAAGATAACCAAGCTCATGCCGTGGTTGTGGGTGGCGTGGTTTGGTTTGGGTAACTTGG
(SEQ ID NO. 313)

.....Rv270T7.seq:.....
TCGGCTAATAATCGTCGACGCCGGCCTCCTCTGCAATCGCCTTGGCGGTGCGCGGGTGTCAACGGTGATCATCACGG
TGCGGATGCTCATTGCGCGCATTTCTGTCGAATCGTTCCCGTATGCCACCTTGACGATGTCCTTCAGATGGACGACGC
CGATGGCCCGCGCGCTGCTGTTATCGGTCCATTCCGCAACGACTAGGGGTGTCCCCCGCGGAGCTGATGCCGTGCGAC
AATGGCACCCACCTCCTCGGTGGGTGGGCACCGTGATCGCGAACCCTTCATCACCGCAGCCGCGGCACCTTGCGG
ATTCGACGGATG (SEQ ID NO. 314)

Clone Rv271

.....Rv271SP6.seq:.....
CTCAAGCTTGGAGGCGTGGCGATCGCGGTCCAAGGCGCGCTCTCCGAGCACAACGAGCGAAGACNGCTCGGCGACGGA
GCCTTTATCGACNTCCGTTCCGGGCTGGCTGACGGCGGCNAAATAATGCTGGACTCGTTGTTGTCGACGGTGCCGTGGC
GAGCCGAGCGCCGTGAGATGTACGACCGGGTGGTCTATGTGCCGCGGTTGGTGAGTTTCCACGACCTGACCATCGAAG
ATCCGCCGCATCCGCTGCTGGCGCGGATGCGCCGGTGGCTCAACTAATTCTACGGCGGGCAACTGGGTNATCCCTTCN
CCACCGTCGG (SEQ ID NO. 315)

.....Rv271T7.seq:.....
CCTAGGTCAACCGTACCGTCATCGGATCGGGGTGACCGCACAGATGGACTGGAGCTTCGGCGAGGTGATCGCCTATG
CCTCGCGGGGGGTGACGCTGACCCCGGGTGACGTGTTCCGGCTCGGGCACGGTGCCACCTGCACGCTCGTCGAAGCAC
CTCAGGCCACCGGAAATCATTCCCGGGTGGCTGCACGACTGCGACGTGGTCACCTCCAGGTGCAAGGGCTGGGCGA
GACGATGCAGACCGTCCGGACGAGCGGCACCTCTTTCCGTTGGCTCTTCGGCCGAATCCGGACGCCGAACCCGACCG
GCGCGGGGTCAACCGGCACCGACGCGGGTGCCGTTTACCCGCGGGTGCACAAATCCCGACGGGTATGGGCTTTGAC
CTGCCGACGGGGGA (SEQ ID NO. 316)

Clone Rv272

.....Rv272SP6.seq:.....
AGCTTGGCGTGACACCAACACAGGGCACTTAAGATGGCAATGCGCCGCTACCTGCACGTTTTTCGCGATGTCAGAGGA
TGCCGAGGGGAGAAACAATGCGAGCACGGCCGCTGACGTTGCTCACCGCTTTGGCGGGGTGACATTGGTGGTGGTTGC
GGGCTGCGAGGCCCCGAGTCTAGGCCGAAGCATATAGCGCGGCCGACCGCATTTCTGCTCGACCGCAAGCGCGACCTCA
GCCGACGCGGTGGAGCTACTGCTGCGCGCCATCACGCCGCTAGGGCTCCGGCGGCGTGCAGCAACGTCGGGTTTGG
CGAACTGCCTACCCGGGTCCGGCAGGCAACCGAT (SEQ ID NO. 317)

.....Rv272T7.seq:.....
TCATGCCGTTGGACCGACCATCGGAGTTAGTTGCCGAACCGCGGGACCACCGCAAGCACCCGGTCTGGTTCGCGCACC
GCGTCGGCCAACCGCTTGAGCACCAACACGCCGAGCCCTCGCCGCGCACGAATCCATCCGCTTGGCGTCGAAGCTG
TTGCATCGGCCGGTCCGTTGACAGCGCCGACCACTTGGACAGCGCGATGGCGGTGAACGGTGACAAGGTGAGCTGCACC
CCGCCCGCAATGCCACGTCGGTTTACGCGAGGCGAAGCTCTGACACGCCAAGTGAATTGCCACCAGCGACGACGAAC
AAGCGGTATCTACGGCGATGG (SEQ ID NO. 318)

Clone Rv273

.....Rv273SP6.seq:.....
GGGTGACTTTCTGCAAGGCGAGGCTACACCGTCGTCGTCGTTGATGCGATAGCCATCCCGTCGGGCTACTCGCCAT
CACCGATCAGCTTCGCCCCGAAGCCGCGGTGGTGATTTCCGCTGCGACCAAATGAACGGGGCCAAACCGGTATTGCT
TACCGGCGACAACCGGGCCACCGCCGATCGGCTCGGTGTTGAGTTGGCAT (SEQ ID NO. 319)

.....Rv273T7.seq:.....
AATCCGAAATCCTGACCGATACTTGAACCTGGTCTCGTTGCGCAATAACTCGTCGGCGTGACGAGCGGGCGCAAACG
TACTTCGGCATCAACGCGTCCGACCTGAATTGGCAGCAAGCGGCGCTGCTGGCCGGCATGGTGCAATCTAACAGCACG
CTCTTCCCGTACACCAACCCGACGGCGCGTGGCCCGGGCGGAACGTGGTCTCGACACCATGATCGAAAAACCTTC
CCGGGGAGGCGGATGC (SEQ ID NO. 320)

Clone Rv274

.....Rv274SP6.seq:.....
TTCCGAATTTCCGGTCCNGGTCATATGACCCTCATGGAAGAAGAAGCGGCCGCCCGCGCCCGTGGGACGGCGAATGA
AAACCCTCACCCAGGCCGATTGAACGCCGACAAGACGGTGGAGCAGGTGGAAGACGTCCTGGACGGTCTGGGTAAGA

CCATGGCCGAGCTGAACAGCTCGCTGTCACAGCTGAACAGCACCGTGGAGCGCTTGGAGGACGGTCTGGACCATCTCG
AAGGTACCCTGCACAGCCTGGACGATCTCGCGAAACGGCTCATCGTGTGGTCGAGCCGGTGGAAGCCATCGTCGATC
GGATCGACTACATCGTGAGCCTCGGCGAAACGGTGATGTACCGCTGTCCGGTC (SEQ ID NO. 321)

.....Rv274T7.seq:.....

NCTCGATCTTGGGGTACGTTTCGATGAGGCTGCTGACCAACAACCCGGCCAAAGCGGGTGGGACTGGATGGATACGGATT
GCACATCATCGAGCGCGTGCCGCTGCCGGTGCGGGCCAAACGCGGAAGAACATCCGTTACCTGATGACCAAGCGTGACA
AATTGGGGCAGCACTTGGCTGGGTGGACGATTTTACGAATCCGTGCATCTGCCCGGAGAATTCGGCGGTGCCCTTGT
GAAGGTGGCGCCGGGTGCCGGATCTGCCGTGCTGGATCGTCTGGTGTGCGGCTGGCGATTGTGCCAGCAGCTGGC
ACGGAAGATCTGCGACGCGCTGTTGGACGGCGCCGCAAGTGCCCGCCGGGTGTGGCCTCGATGACCGACTGTGGTT
CGGGTGCTCCGCGCATCGATAT (SEQ ID NO. 322)

Clone Rv275

.....Rv275SP6.seq:.....

TCATCCCGACCAAAACGCGAGCTAGGTCGGCATCCGGGAAGCATCGCGACACCGTGGCGCCGAGCGCGCTGCCGGCAG
GCCGATTAGGCGGGCATATTATCCCGCCGCGGCTCCCGGCTCCGAGTACGGCGCCCCGAATGGCGTCAACGGCTGGTA
ACCGCTCTTGCGCGCCTGGGCGGCGGCCTGCCGGATCAGGTGGTAGATGCCNACAAAGCCTGCGTGATCGGTCATCAC
CAACGGTGACAGCAGCCGGTTGTGCACCAAGCGGAACGCCACCCGGTCTCCGGGTCTGTCCAACCGATCGACCGCC
CAAGCCCATGAACAAACCCCGGCATCACGTTGCCGATCGGCATACCGTGA (SEQ ID NO. 323)

.....Rv275T7.seq:.....

TTGGCGGGTTGGCCAGCAGCCCGCCGGTGACGGCGACGATGCTGGGCTGGTTGCGGCCCTGCGCCACCGCGGCTTGC
ATGCTGGTTGGCTGTCTTGGGACGATCCCGAAATAGTCCACGCGGATCTGGTGATTTTGGGGCTACCCGCGATTACC
CCGCGCGGCTCGACGAGTTTGGCCTGGACTACCCGCGTGGCCAATCTGCTGAACTCGCGGCCGGTGGTGGCCTGGA
ATGTCGAGCGCCGTTACCTACGTGACCTGATGGATCGGGGGGTGCCGACCGTGCCCGGCGATGTGTATGTGCCGGGAN
AGCCGGTCCGGTTGCCACGCAAGGCCATGTCTTCGTGCGTCCGACCATCGGTACCGGGACACGGCGCTGTATTGCC
GGTTCGCTGCCGAGTTCGTGCGCAACTGCACGNGCGGGCCAGCGGTGCTCGTTCCNCCGGAGGTTCCGGTGACG
ATGATCGTGTGGTCTCCCT (SEQ ID NO. 324)

Clone Rv276

.....Rv276SP6.seq:.....

GTAGGAGAGAACAAGACCGTCGATAGGACACGTGTTACGCCGGTAGCTGTCATTGGTATGGGGTGCCGCTGCCGGGG
GGCATCTACTACCCGATCGGTTGTGGGAGGCGTTGCTGCGGGGCGACAATCTGGTCACCGAGATCCCGCCGACCGC
TGGGACATCTACGAGTACTACGACCCCGAACCCGGCGTGCCCGGACGCACCGACTGCAAATGGGGCGCGTACCTCGAT
AACGTCGGCGACTTTGATCCCGAGTTCTTCGGGATCGGGGAGAAAGAAACGATAGCGATCGATCCGCAGCACCGCTTG
TTGCTGGAACCTCTTGGGAAGCCATGGAACACGGCGGGCTAACACCGAACCATATGCCTCCCGACANGGGTTTTCTG
GGGGTT (SEQ ID NO. 325)

.....Rv276T7.seq:.....

CGAACTGAGCCCATAGAAAGGCAGCGACTAATTCGCTGGGCAAATAGGAAGACCCTTTGTCCTGCCACGTATATTTGT
CGACCTCGTTGCGAAGGAAGCGGCTGCCGATTGGTGCCCTTTTCCCTGGAGAATCTCTGCCCGGAGCAGGAAGTCTTAT
GAGTTGACAAGCAGGGGCGCCGCTTCGCCGAAATCACATTTTGGTCTCGTGAAATGAGAGCGCTCCCAGGTGCGC
GATGCTGCCGAGCGCCCGCCACGATACGACGCCATCGCGCTTGGGCGCGCTCTTCGACCACCGCCAGGTTGTGGTG
CGTGGCGATCTTCATGATCGCGTCCATCTCGCAGGCCACCCGGCATAGTGAACGGGGACCATGGCCTCGGTTGCGGG
TGAA (SEQ ID NO. 326)

Clone Rv277

.....Rv277SP6.seq:.....

CTTAGACGCCACCTCCGGGCGGAGCTCCACGGGGTGGATAAGTACGGCCGGATGTGGCCGCAATGGGAAGTTGTTGCC
CGCTTGACTGTCCGGGTTAACGCCGATTCCACCACATCCCTTGCGAAAGGCCGTTGGGTT (SEQ ID NO. 327)

.....Rv277T7.seq:.....

GATCGCGATCGTCGATGTGGCCATCCGGCTTGGCGTCGACCCGCGTAAGGCAGACCAGATGGTTCGCGGCACGGTCAA
CCTGCCACACGCACTGGTAAGACTGCCCGCGTCGCGGTATTCGCGGTTGGTGAAAAGGCCGATGCTGCCGTTGCCGCG
GGGCTGATGCTGTCCGATCGAGATCTGATCGAGAGGATCAGGGCGGCTGGCTGGAATTCGATGCCCGCATCGCGAT
ACCGGATT (SEQ ID NO. 328)

Clone Rv278

.....Rv278SP6.seq.....
AGCTTACGCCGCTTTCGCTTCNGATTGGGACGCCGCATCGAAAGCGCAGTTGGAAGCGCGGCGCCCGGCTGGTTCGAG
CTGCTCAAGCAGCCGCAATCCCAGCCCATGCCCGTTGAGGAGCAAGTGGTTTCGATCTTCTGGGCACCGCGGTCAC
CTGGACTCGGTGCCCGTCAAGGATGTCGGCGGTTTCAAACCGAATTACTGGACCACATGCGGGC (SEQ ID NO. 329)

.....Rv278T7.seq.....
CGACGGGACCTCGTCGCATCTCCATAGCCCCGCCACACCTTCAGTTGCTCACCAGGAATCCAACCGGTATAAGGTTCGGC
GAAGCGCTCGGCATTGGTCATCGGGATATGCCGCTCGGGACGGTCAGATGCCCTCGGGTCCNGCCAGCACTCCTCAGG
CTTCGTTCGGGGTGGTCGCGACCGCATGGGCCACATCGCATTACCCAGGTCTGCGCGAATCACCAGCACGTANACGGTT
CCTTTCCTAAGCAACACCGAAATTCAGGACCCGAATGCTCCGGGAAAACATGTCACGGTAAGTCCGGTATTCCGGGT
ACCGGTTGAGCATTGA (SEQ ID NO. 330)

Clone Rv279

.....Rv279SP6.seq.....
CGGCATCGGTTTGGGCTGTCACCAGCAGTTGGTAGTTCTTCACTACTGTTGTTTCGAGCGTCGAGCCGCCGCGCGTGT
GAGGTGCGCCGACGCGTACCCGCCAGGCCGGTCAGGGTGCCCTTCAGTCCACGCNGCTGTGGTTCGGCTAACCGCTTA
TCTTCAATCGAGACNATCGCCAGCTTCATCGTGTGGCGATCTTGTCCGAGGGCACCTCGAACCGGCGCTGCGANTAC
AGCCACGCGATCGTGTGCCCTTCGCGTCGACCATCGTCGATACCCGAGGCACTTGCCCTCGAGCAGTGGGCCGAT
CCGTTGGCAACGACCTCAGAGGCAGGATTGGACATCAGCCCTAGCCCGCCTGCG (SEQ ID NO. 331)

.....Rv279T7.seq.....
CCGTCGANGCCGCCGACTTGGCTTGACCGACCAACATGGCCTGAGGGTGTTCAACAAGACCGTGGCCGACGGGGCTG
AACATCACCATGAGCGGCATGAGCCACGCCACCGAGTTCATCATGTTGATCGCCGAAAACCATTTGGCGGGTAGCGGAA
GAACGGTCGAGGTGCTCTACACCGAGTATTCGAAGTCGAAAGGCCAACCCTGCTCAACGGCGTCAACATCATTTTCG
ACGGGTTTCTGCGAGGGAGGATGCCACGATGAAGTGGATCCAGGTGCTGTTGATCGCGTCGATCATCGGGTTGCTGTT
CTACCTGTTGCGGTGCGGCCGAAGCGCGCGGTCCGTGCCTGGGTCAAGGTGGGCTATGTCTTGTTCGTGCTCCCGGCA
TCTATGCCGTGCTGAGA (SEQ ID NO. 332)

Clone Rv27

.....Rv27SP6.seq.....
TTACACGNCTGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGAC
CATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTTTTCGAGCGTCGCGCGGGGCGAGCTTCGCCGG
CAATTCTACTAGCGAGAAGTCTGGCCCCGATNCGGATCTGACCGAAGTCGCTGCGGTGCAGCCACCCCTCATTGGCGAT
GGCGCCGACNATGGCGCCTGGACCGATCTTGTGCCGCTTGCCGACGGNGACGCGGTANGTGGTCAAGTCCGGTCTACN
CTTGGGCCCTTTGCGGACGGTCCCAGCGTGGTCGCGGTTGCGCCGCGGAAAGCGGCGGGTCCGGTGCCATCAGGAATG
CCTCACCGCCGCGGCACTGNACGGCCAGTGCCGCGGCGATGTGNGCCATCGGGACATCATGCTCGCGTTCTACTCTCT
CGACC (SEQ ID NO. 333)

.....Rv27T7.seq.....
CAGGCATGCAAGCTTTGTACACCAAGTGTTCGACAGGCGCTCCATCCGGCGAGTGGATACTCCAGCAGGTAGCA
GGTCGCCACCACGCTGGTCAGTGCGGTTCAAGTTCGCTTTCGCGGCTGACGAGCCAGTCCGGGAAATAGCTGCCCTG
GCGCAGCTTGGGGATCGCGACGTCGATGGTTGCGGCACGGGTGTCGAAATCAGGTTGGCGGTAGCCGTTGCGCTGATT
GGACCGCTCATCGTGCCTTCGCGGTAGCCCGCCCCGCACAGGGCGTCGGCTTCAGCCCCCATCAAGGCGG
(SEQ ID NO. 334)

Clone Rv280

.....Rv280SP6.seq.....
AGCTTAGCCAGTTTCTACTCTTGGGCCACACCCACAGTGCTTCGACGGTACGGTCACCCATGATGGCCATCCAGT
TGGCATCGGTGAGCTGATAAATGCCAGCTGGTTTCGCCAACCCGGTAGCGATCTTGGCGCGCTGCTTGTGTCAGTGA
TACCTATCGAGCAAGACAGCCCGGTTTGCAGCAAGATGACTTTTCGGATCTCTTCGGCGACTTCGATGGGGTTCGTCGG
GAGTCCCGGGCGCCACCGCGAGGTAAGCCTCGTCCCAGCCCCATACCTCGACCGGGTATCCCAGGTTCGCGCAATAACG
CCACCACCTCTCGGACGCCGCGTGTAGGCGGCTGGGTTTCGACGGCAAGAAGTGGCCTCAGGGCATCGTCGGCGCGG
TCCCAACGGCNTGCCGGCGCGCACACCGTAGGCGCGGGGCTC (SEQ ID NO. 335)

.....Rv280T7.seq.....
CCGGCGGAAGTACAGCGTGCTGGTGGTTCGGCATGGCACCGCGGGCAGCAAAGCGCACTTCTCCGGGGACGACAGCAA
GCGACCGCTAGACAAGAGGGGTGCTGCGCAGGCAGAAGCGTTGGTACCACAGCTGCTGGCGTTTCGGCGCCACCGATGT
TTATGCCGCCGACCGGGTTCGCTGCCACCAGACGATGGAGCCACTCGCCGCGGAAGTGAACGTGACCATACACAACGA
GCCCACCTGACCGAAGAGTCTACGCCAACAACCCCAACGCGGCGGACACCGAGTGTGACAGATCGTCGAGCAAGT

AGGCACACCCGTGATCTGCACGCAGGGCAAGGTCATTCCCGATCTGATCACGTGGTGGTGCGAGCGCGACCGTGTGCC
CCCCACAGTCCCGCAATCGCAAAGGCAGCACGTTGGTGT (SEQ ID NO. 336)

Clone Rv281

:::Rv281SP6.seq:::

GTATGGTCAGCTGTCCATCCGGCGCTGTCGGCCGAGCTGCCAGATCTCGTCAGCCGTAACCGGGTTGCGGGATCCACG
CGTGCGGGTTGTCTAC (SEQ ID NO. 337)

:::Rv281T7.seq:::

CCGACTTTCGCGGGTACCCGCTCAACTTTGTGTCNACCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAACT
ACTTCATCCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACT
ACATCATTGCGACGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACC
TGGTTCAACAACTTGAAGGTGATTGTTAACCTGGGCTACGCGACCCGGCCTATGGTTATTGACCTCGCCGCCAA
TGTTGCGACTCCGTTGCGTTGTTCCAGAANGTCAGCCG (SEQ ID NO. 338)

Clone Rv282

:::Rv282SP6.seq:::

GCACCGATGTCGGCGAGCACTTCGTCAACTTCCAGGGGTGCCCGCACCAAGTATTCGACGAGTATTCGGTCGGGCC
GCCGCCGCCGGTGCGCGGCAGGTGGTCATCCTGGCGCGGGGGCTGGGACTCGCGCGCGTACCGGCTGCCTCGGC
(SEQ ID NO. 339)

:::Rv282T7.seq:::

TGCACCAACTTACTGAGCATGCTAACGCTGGTTCGTGCGGGTCTTGTTCGCGGTGTCGGCAGGGCACACGCTCGGGG
CGTAGCTGGGAGAGGCCCGGTCAAGCCCGGAGAGCAGTGCTCAGTCCGCCAGCTTGACCGACTTTCGATGAGAACGC
GCTTCTCGCGTATTGAAGTGGCGTGCTGACGGTCGCTGAGCAGCGCTCGCCGAGTGGCGCGCTGATTCTTTCATCG
AGCCAGGACGCGCATTCGTGTTCCGCCG (SEQ ID NO. 340)

Clone Rv283

:::Rv283SP6.seq:::

AGCTTACGGCCGGTCGACGCGACGAGTGGTTCATGACACCACAAACCGTCAACGCCTACTACAACCCGGGGATGAACG
AAATCGTCTTCCCGCAGCGATTTTACAGCCACCATTTTCGATCCGCAGGCCGACGAGGCCGCCAACTACGGCGGGAT
CGGGGCGCGTGATCGGGCACGATGATCGGGCACGGTTTCGACGATAGGGCGCCAAATACGANGGCGACGCAATCTGGT
CNATTGGTGGATCGA (SEQ ID NO. 341)

:::Rv283T7.seq:::

ATGTCGTCACGTACCAACAATCGCGAGGACCAATCATGCCGCCAGGGCGGCCAACCCAATGGTGGCCGCGAAGCGG
CAGCTCGATCGCAGCGCGGAGGTGCCGGCCGCCAGTTGATTACGAACAGGGTGAGGTCTAGGCCGGCAGGATAGTG
ACGAACGCAAGACCTATATCTGCCGTGGAGTAAGAAATCGAGTAGCCGGTCGACCAACGGAAGCGAAAGTGTCGCGA
TGTTGATGAGCGTCGCCGGTTGTGGCGCGGTGGC (SEQ ID NO. 342)

Clone Rv284

:::Rv284SP6.seq:::

AGCTTACACAGCGTGCCGATGCTGTTTCGCNACACCTCCCTACTATGCGCAATTGCGCGACACGGGTGGCATCAACACG
GGCGATAAGGTGGACATCGCTGGGGTGAACGTCGGGCTGGTGCGCTCGCTGGCAATCCGCGGCAACCGCGTGTGATC
GGATTCTCGTTGCCCGGCAAGACAATCGGGATGCAAAGCCGGGCAGCAATTGCGACCGACACCATTTGGCCGTAAG
AACCTGGAAATCGAACCCCGCGGTTCCGAGCCGTTGAAACCCAACGGTTTCCTGCCGTTGGCGCAGAACTACGCCA
TACCAAATCTATGACGCGTTCGTC (SEQ ID NO. 343)

:::Rv284T7.seq:::

CTGCCGCGGTGGCGGTGACGCGCTGGCAAGTACCGCACCGCCGTCGCGTTTCATCGGCAGGCTCCCCGAAAAGGGCC
CTGGCAACAGAAGGTGATCAATGAGCTCCCGCAGACCTTCGCCGATCTGGGACCGACATACGTGAAGTTCGGCCAGAT
CATCGCTCCAGCCCGGAGCATTCGGTGAGTCGCTGTCGCGGGGAATTCCGCGGCTGCTCGACCGGGTGGCCCGG
CAAAACCGACGAGGTGCACAAGCTCTTCGTCGAGGAACCTCGGCGACGAGCCGGCCCGGCTGTTGCGCTCCTTCGAGG
AAGAACCCTTCGCTGTCGCTCCATCGCCCAAGTGCATACGCGACCTGCGCAGCGGCGAAGAAGTGTGGTCAAGATC
CAGGGCGGGCATCCGCCCGCGGTTT (SEQ ID NO. 344)

Clone Rv285

:::Rv285SP6.seq:::

GATCGTGCCGGCCCCCGGCGGCAGTAGCAGATCAGCTCGTCAAATCGCGGCAACCAGTCCAGTTCGATTTCATACG
GGCGCCGTCAATCAACTCTGCGAACATCGCGATCGGCACCGGAAACCGGCGAGCCGCGTCAGCCAGCGCAACCAGCAC
CGGGATCGGATGAATCATCAATATTATCAAGTGATTTCTGATGGCATCGAGCTCGGTGATCTTGGTCTCGGGGGCCA
GCTCGCCGTCGGCGACGTCTGTCGATCCGGCGGCCGAGCGCATAGACCGCAAATAGTGCCGCTCGCTTTTCGCGCGGCA
AGAGTCGGATGCCGTAATATANGTTTCTGGCGGCCGTGCGCGTGATCNACTCGGTGATTTCGATACGCCTGTTTCATCTC
GGTCATGCCGTCTC (SEQ ID NO. 345)

::::::::::Rv285T7.seq::::::::::
GGTGGCGCAATGACCGAAACACCCAGCCCCGAAACCCCGGCGGCCCGGCGGCCCGGCGCACAATCGTTCTGTGTTG
GAGCGGCCCATCCAGACCGTTGGGCGCCGTAAGGAGGCCGTGGTACGAGTGGGCTGGTCCCGGCACCGGCAAGTTC
GACCTCAACGGCCGAGCTTGGAGGACTACTTCCCAAACAAGGTGCACACAGCAGTTGATCAAGGCACCCCTGGTCACC
GTGGATCGGGTGGAAAGTTTCGACATCTTTGCCACCTGGGCGGCGGCGGCCGTCGGGTTCATGGCCGGCGCGCTGCG
CCTGGGTATCGCCCGGGCATTGATTCTNGTATCGCCGGATGACCGGCCGCGCTGAATAANGCCGGCTTCTTGACCGT
GATCCACGCGCCACCGAACGCAA (SEQ ID NO. 346)

Clone Rv286

::::::::::Rv286SP6.seq::::::::::
CACATAGATTACTCAAGCTTCGAACAGCGGCCTTATCACGTATCCCCGCTGAGACCTTGACCTTAGGGCCGAAGT
GACTTCGCTGCTGCTATGCCGACACCCGATTTCCAGACGCTGCTGTACACGACGGCCGGCCGGTGGCCACCATCAC
GCTCAACCGCCCGAACAGCTCAACACCATCGTCCCGCCATGCCCGACGAGATCGAGGCCGCTATCGGGTTGGCCGA
GCGCGACCAAGGACATCAAGGTTCGTGCTGCGCGGTGCCGGCCGCGCTTCTCCGGCGGTACAATTCGGCGGCGG
GTTCCAACATTGGGGGCAT (SEQ ID NO. 347)

::::::::::Rv286T7.seq::::::::::
TCAGGACGCTTATGGTTGGCAGATGGTCGCCCTGGCGTCAATACGCGGAGCGCATGAGCTCACCGGTTCCGAACAA
CGTATCGAAGAACGTGCGACTGCTGGCAGATGGTATCTCCGATGTGGTTGTAATTTGTATCCCAACTCTAAGTGTGCT
ATCGGATCAGCGTGAATATCGAGATATTGCGAATGCGATGACAGGCCGCCATTGGTTTATTTCGCTTACGCTTCCCGG
GTTTCGATTCTGCTGATGCACTGCCGCAAACGCGGATATGATTGTTGAAACCGTATCTAACGCAATTATTGATGTGGT
AGGCGGCAGCTGCCGTTTTGTGCTGTGCGGCTATTTCATCGGGTGGGGGTGTTTGGCTATGCCCTCTGCTCCCAT
(SEQ ID NO. 348)

Clone Rv287

::::::::::Rv287SP6.seq::::::::::
CGCAGCTGTGCGCGATCTGGTCCGGAATACCTAGCTCCAGGTTCTGAGTGAGATGAGTGCGGCCATCGAAGTGTGT
CAATGTACTCCAGGATGTCAGGTGCCAGGCCGCTGGCGAGGATCTTGGGCACCGCCGCCATGACTTGGTTCGAAGTCGG
CGAACGGGGCGAGCACGCTGGCGTCTGTGTC (SEQ ID NO. 349)

::::::::::Rv287T7.seq::::::::::
GTAGTTCGTTTCATCCAAACAGTGCGGTACCGCTCAAGCGGATCACCGACTTCACCGGGCGCGATCCACCCAGCC
ACCGCATGCTTATGTCCTTCGGGTGGCGGCCACCGTGGGTCAACTCAACTATCCGACGCCGCACTGAAGCATCGACAG
CAATGCCGTGTATAGATTCCCTCGCCGGTCAGAGGGGTCCAGCAGGGGCCCGGAAAGATACCAGGGGCGCCGTC
GGACCGA (SEQ ID NO. 350)

Clone Rv288

::::::::::Rv288SP6.seq::::::::::
TCCGCTCGCTTCTCCGAGAGGTTGAGTGCCAACGCTCTGCCGATGCCCGAAGCCGGCCCCGGTGATGACGGCGACCTT
GCCTTCGAATGAGCTCATTTGACTACTCCCCGTGGTTGTCCCTGCGATTGGTGGAGGTGGCCGCGCAGCCTTGCCCCG
AGGTGGGCGATCGCGTCTCGGGCTTCGGGGAGCAGACTGACCTGCAGATGGAAGTCGTGCCACATGCCCGCGAACCGG
CGATGCTCGATGCTTGTTCGAAGCGGCGCAGGCGGTTTCGATCTTGTCCGCTCAACACNGATCGGATCGTCGCC
CGGGTCTGCATGACGAATGGGCG (SEQ ID NO. 351)

::::::::::Rv288T7.seq::::::::::
ATGGGAGGCCACCGATTACCATCTTGACACACCGATTCCGGGCTATTGATGTCCACGTTCCGGTCCGCGAACCGCGCT
GTGGCTGCTGCTGGCCAAAGGCGGAGGCGATACCGAAGTCAGTGCCCAAGCTTGGGTTCCACGCTCGCGCAGCCACGC
CGTCACCTTTCCACGAGACCTCACCTGCCGATCCGAAATGGAATCGGCCGTGACGGAATTGGCGCAGCGAACACTCAA
CGAGGTGGTGGCTTCGTCGCGAACCGTCAACCGAGTCGCGGTCAACGTCGCGCAGCGGACGTTCTACACCCGCAACAA
GATCCGAAAGCTGCAAGCTCCAGCACCGATCCGACGTCATCACCGCTGCCGCCCGGACGTTCTTGAACCTATTGC
AGCTGGAATCGGCCGTCCGGTTGCTGGGAATTGCNGTTAAGAACTGGGCCT (SEQ ID NO. 352)

Clone Rv289

.....Rv289SP6.seq:.....
GCTTTGCGCGCTTCTCCGAGAGGTTGGAGTGCCAACGCTCTGCCGATGCCCCGAGCCGGCCCCGGTGATGACGGCGACC
TTGCCTTCGAATGAGCTCATTGACTACTCCCCGTGGTTGTCCCTGCCGATTGGTGGAGGTGGCCGCGCAGCCTTGCCC
CGAGGTCGCGGATCGCGTCGCGGGCTTCGGGGAGCAAACCTGACCTGCAGATGGAAGTCGTGCCACATGCCCGCGAACC
GGCGATGCTCGATGCTTGTTCGAAGCGGCGCAGCGGTTTCGATCTTGTCCGCGTCAACGCAGATCGGATCGTCGCC
CGCGGGTCTGCATGAAGAAT (SEQ ID NO. 353)

.....Rv289T7.seq:.....

CTCACGCAGCCACGCCGTACCTTTCCACGAAGACCTCACCTGCCGATCCGAAATGGAATCGGCCGTGACGGAAATTG
GCGCAGCGAAACACTCAACGAGGTGGTGGCTTCGTGCGGAACCGTCACCCGAGTCGCGGTACCGTGCGCACGGCGAC
GTTCTACACCCGACCAACATCCGAAAGCTGCAAGCTCCAGCACCGATCCCGACGTCATCACCGCTGCCGCCCGGCA
CGTTCCTTGACCTATTTCGAGCTGGATCGGCCGTCCGGTTGCTGGGAGTGCGGTTAGAACTGGCCTAGAAACCGGCGG
GCACACCGCACCTGGGCGGGN (SEQ ID NO. 354)

Clone Rv28

.....Rv28SP6.seq:.....
TGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG
CCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCAGCCACC
ACNCGCGGGTCGGGCGCCGGGCCCCGGGTCGCCANGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACACCCGGC
TGCGCTACGTGAGCCATACCGGGCGGAGCTACATCGGCTCGGCCGCCAGTGTTGCGGCCCTCTTTCGAAGTCGAAG
TCGATACCGATTGCGCATCCGCGGCCGCA (SEQ ID NO. 355)

.....Rv28T7.seq:.....

CAGGCATGCAAGCTTCACGTCCGTACGGCTCGGGTACGCTTCGGTTCGCAGTGTGCGAGTGATAGATGACGACCGGGAC
CTCGTCTGCATCTTCCATAGCCCGCCACACCTTCAGTTGCTCACCGGAATCCAACCGGTAGAAGGTGGCGAGCGCTC
GGCATTGGTCATCGGGATATGCCGCTCGGGACGGTCAGAACCCTCGGGTCCGGCCAGCACTCCGACGGCTTCGTCGGG
GTGGTCGCGACCGCATGGGCCACC (SEQ ID NO. 356)

Clone Rv290

.....Rv290SP6.seq:.....
GCTTGTCTATCGTCCCGGCCAGGTCCGGCCAGTCAAGGTGGAAGGCCAGTCCGGTCTCCTCTCCGACTACGGCCAAGA
ACTGGGCGACGGTGTGAGTGCAGACCGGAACTGGTGGCGCCCTAGGCGAGCGACCGCCTCACAACCGGCGGTGA
CCGCGTTCTGGTTCGTGCACCATCGAGCCGTGCCAGCCCGGCCGCGTCCGTCAGCCGCATCCACTGGATGCCCTTCT
CGGCGGTTTCAATCAGGTACAGGCGACGTTGCCACCATCGTGCCGGGCGACGGTTAGCGAGAAACCGCCGACTTCAC
GATTGCCCTCGGTGATGCCGTGAAACAGATCGGGCCT (SEQ ID NO. 357)

.....Rv290T7.seq:.....

GCGCGCCATGTTGAGGTTGTCCGACGGTGACGACGGTGAACCACAACCTGTTTGACCTGTCCGCACACACCGTGTGGAT
CGGCGAGCGGACCCGACAAATCGATGGCGCGCACATCGCGTTTGCCAGGTGATTGCTAATCCGGTCCGGGTCAAGTT
GGGCCCCAACATGACCCCGAACTGGCGTGGAGTACGTGAGCGGCTCGACCCGCAACAATAAGCCGGCGGCTGAC
TTGGTGAGCAGGATGGGCAACCACAAGGTCCGCGATCTGTTGCCACCGATCGTGGAGAACGTCCATGCCACCGGGCAT
CAGGTCACTTGGC (SEQ ID NO. 358)

Clone Rv291

.....Rv291SP6.seq:.....

TTGCCTTCCATGCCGAGCAAGGTCGACTCAGCGATGACGAATTGTTCTTCTTCGCGGGTGTGCTGCTGGTTGCGGGC
TATGAGAGCACTGCTCATATGATTAGCACATTGTTTCTGACGCTGGCCGACTATCCAGATCAGCTGACACTCCTTGCG
CAGCAACCAGACCTGATCCCGCCGGCGATCGAGGA (SEQ ID NO. 359)

.....Rv291T7.seq:.....

CGACGCTGGGCCCAACTGCGACCACCGGTCCTGGTATGGCAGGACATGGCCGGGTTACGCGGCGCCAATACCG
(SEQ ID NO. 360)

Clone Rv292

.....Rv292SP6.seq:.....

TAACGACTCGGGTCCAGCGACCGCCAAACACNAACGGCCGACNACGTGGGCCAGGGTCGCGGCCCTCCCTACAAAC
AGGATCGGTTGCCTGCGAACGACAGGCTCCGGTGGCGGCTTGGGCGCCGTGCTCGTCCAGCGTCCGGTCCCGGGTCCG

CCGGCGACGCTTGTTCCTCCATACTCGCCCCCTAATCTCGAGGCAGCCCGTACCCGCAGGCAACCTCCCAAAAATGC
AATCCCCCAAAATGCAATGCGTCNAGCTATTTCTCACACCGACCGCTAGTTGCGGATCANAAATCCGTTGGGCGCGGA
(SEQ ID NO. 361)

::::::::::Rv292T7.seq::::::::::
CNTGGCGGTGGGTGCGGTGTCGAACACGACCACACTTCTTTGCGGTTGCGTGATCTCGACACCGGCCGCGAGCCGACC
ACCATGCGCGCGTAGATCGGCGATCAGCGCGTCGGCTATCGCCTGGGTGCCGCCACCGGAATCGGCCAGCCGACCGA
ATGGGCCAGCGTTGCCATCATCAGTCCGGCGCCGGCCGACACCAAGTGACGGCAACGGTGAAATCNCGTGGGCGGCAAC
GCCGGTGAACAACGCGCGGGCATCCTCGCCGCCAGCGACCGCCAGGCAGGGGTGCCCTGGGCCAGCATCCGACGCC
GAGACNCAGGACCGANCCAGTG (SEQ ID NO. 362)

Clone Rv293

::::::::::Rv293SP6.seq::::::::::
GCTTTTCNGATCGCAGCGAGTCGTACCCGCGCCGGTCACCTTCGTGGATATCGCCGGCCTGGTCAAGGGGGCGTCCGA
GGGAGCCGGGCTGGGTAACAAGTTCTTGCTCATATCCGGAATGCNACGCCATTTGTGAGGTGGTGCGGGTGTTCGT
CAACAACNACTTGACTCATGTACCGGACGGGTCGATCCCCANTCCGACATTGAGGTGCTCGANACCGAGCTGATCCT
GGCANATCTGCAAAACCCTGGAGCGGGCCACGGGCCGGTGGAGAAGGAANCGCGCACCAACAAGGCGCGCAAGCCGGT
CTACGACGCGGCACTGCGTGCCAGCAGGTGCTCGACGCCGGCAANACGCTGTTCCGCCGCGGGGGTGGATGCCG
(SEQ ID NO. 363)

::::::::::Rv293T7.seq::::::::::
GTCGTACGCCATTNGTCGGTGTGCGCATACCACTACGACGCGCCGGGCACCTGACGCGGCGGCCGCGACCACTCGGTG
GCCATCGCCATCGTCTGCCACCCGGTCAACGGACGCACCTTCTCCTGGCCGACGTAGTGCGCCACCCGCGCCCGTTG
CGTCCCATCNATCCGGTCAACATGAGCAGCGCCAACACCGAGCGGTACATGACATCGCTGTGGAACCACTGACAGATT
CCGCGGCCCATGATGATCATCGACCGTCTCCGGATTGCGTTCGCGTTGCGGGCGAAATTCCTTGGCAAACCGGATTGC
CTGCGCGGCCGCGCACACCGGTGATCGACTCCTGCCAGGCCGGGGTGTTCGCTGGGTTCGGTTCGTGGTACCGGT
(SEQ ID NO. 364)

Clone Rv294

::::::::::Rv294SP6.seq::::::::::
GCGAGGCGGTATCGCTTCCCGTCTACCGGCGACCGCCAGCCGAGAAGCTCGTTTTCCAGTGTTGCTGGGGATTCTC
ACGCTGCTGCTGANTGCGTGCCANACCGCTTCCGCTTCGGGTTACAACGAGCCGCGGGGCTACGATCGTGCGACGCTG
AANTTGGTGTTCTCCATGGACTTGGGGATGTGCCTGAACCGGTTACCTTACNACTCCAAGCTGGCGCCGTCTCGTCCG
CAGGTGCTTGCTTGCATAGCCGGGAGGCCCGGATCCGCAATGACGGATTCCATGCCAACGCTCCGAGTTGCATGCGG
ATCGAATACNAATTGATCACCCA (SEQ ID NO. 365)

::::::::::Rv294T7.seq::::::::::
TGGGTCTTGCCGGCGAGCCAGCGAAGTCGCTAGCGTGCGCGTGTTCCTTGGCTTCGGATCTATCCTCGTTACATGAC
CGGCACCGTGTGGACGTGACTGGCGGCCGGTTCATATGACACCGAGATCATTGCCACGGTACGGAATTCGTCAAGA
AGGAAATCTTTCCNATGCACCGGCCCTCGAACGTGGCAACAGCTACCCGCAAGAAATCGTCGATCGGCTGGGTGTTA
TTGGCTTGCTCGGTGCGCGGCTGCAAGGGTATCGACACCACCGAGTTCATTCTCGGGCGTGCCGGCGCATTCGAGCTG
GCGGTGCGCGCTGCCAGCACCGTCATAAGTACTTGANGATGGTCAAACGTGCGACGAACCGCCACCACGTGCTGCC
GAACGG (SEQ ID NO. 366)

Clone Rv295

::::::::::Rv295SP6.seq::::::::::
TAGATGCCCAAGCTTGCCNTTANAGACCTCGTCGACCAAGCACGGACGCGACCGTCGAAGGTGGCGAATCCGGGCTTG
GCGTCNACCCGCGTAAGGCAGACCAAGTGGTTCGCGGCACGGTCAACCTGCCACACGGCACTGGTAAGACTGCCCGCG
TCGCGGTATTGCGGTTGGTGAAAAGGCCGATGCTGCCGTTGCCGCGGGGGCGGATGTTGTGCGGAGTGACGATCTGA
TCGAGAGGATTGAGGGCGGCTGGCTGGA (SEQ ID NO. 367)

::::::::::Rv295T7.seq::::::::::
TCTCCACGGCGTGATCAAGGTACCGCCGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGCTTGATGTCTGCGTTAG
CGCCGGATTCCACCACATCCCCTTGCGAAAAGTCCGTTGGGTGCAATGATGTAGCGCTTCTCCCCATCGAGATAGTGG
AGCAACGCAATCCGTGCGGTACGGTTCGGGTCGTACTCGATGTGCGCGACCTTGGCGTTGACACCATCTTTGTCATTG
CGGCGAAAAGTCGATCATCCGGTAAGCGCGCTTATGACCGCCGCTTTGTGCCGGTNGGTAATCCGGCC
(SEQ ID NO. 368)

Clone Rv296

.....Rv296SP6.seq.....
GCCCCGTTTCGATCGGGCATGTCCGCAGTCGTCTTACCGGAGGCGGTCTGTGGCCGCGCTAATCGGCGTCGGCGCCGAC
AAGATGTGGGATATCCGCAATCGGGGCGTCATCCCTGCGGGCGCGCTCCCCGCGTCCGAGCCTTCGTGACGCAATC
GAGGCAAGTCACGACGCGGATGAGGGGCAGCAGTGAATTACAGCGAGGTCGAGCTGTTGAGTCGCGCTCATCACTGT
TCGCGCGAAACAGTCGGCGACCGGGGTTGGATGCGGGCACCACACCCTACGGGGGATCTGCTGTCTCGGGCTGCCGAC
CTGAATGTNGGTGCGGGCANCGCCGTATCNACTCCCGTGAACACAGCCGGGGC (SEQ ID NO. 369)

.....Rv296T7.seq.....
CTCGGCGTGGATATCGGTGTAGCCGGCGCCGGTGAANGTCGGCTCCTTACGTCCACTCGACAACAGCTCATAGCGATC
CAACCAGTANGCAACCGCCTTCAGCAGTACAACCGCGCCGGCGAACACTGCGAGTTGAACGCGAGCTGCCTGGGTCAG
CATGCCCTCTGCCGTTGTCTAGCCGAAGGCCGCCGAACAGGTAATGCGTCAACAGGCTCGCTAGAAACGCCAGAACCAC
GGCCACGAACAGCCAGTTCAGCACCGACCGGTAGAACGGCAGATCGAAGACGAAAAACCCAATGTCATAGCCGAATT
CGGGGTCCACGATGCCAAAGGTGCCCCGTGTACAACACTGAACCTTCACCCA (SEQ ID NO. 370)

Clone Rv29

.....Rv29SP6.seq.....
TCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAA
GCTATTTAGGTGACACTATAGAATACTCAAGCTTCAGTCCGTACGGCTCGGGTACGCTTCGGTTCGAGTGTGCGAGT
GATAGATGACGACCGGGACCTCGTCGGCATCTTCCATAGCCCCGCCACACCTTCAGTTGCTCACCAGGAATCCAACCGGT
AGAAGGTGCGCGAGCGCTCGGCATTGGTCATCGGGATATGCCGCTCGGGACGGTCAGAGCCCTCGGGTCCGGCCAGCA
CTCCGACGGCTTCGTCTCGGGTGGTTCGCGACGCGCATGGGCCACCATCGCATTACCCAGGTCTGCGCGAATCACCAGCA
CGTAGACGGTTCCTTCTTAAGCAACACCGAAGTTTCAGGACCGAATGCTCCGGGAAACATGTCA (SEQ ID NO. 371)

.....Rv29T7.seq.....
CAGGCATGCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCAGCCACCACGCCCGGGTTCGGGCGCCGGGCC
CGGGCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACCACCGGCTGCGCTACGTCGAGCCATACCGG
GCGGAGCTCCATCCGCTCGGCCGCCAGTGTCCGGGCCCTC (SEQ ID NO. 372)

Clone Rv2

.....Rv2SP6.seq.....
CCTGCATCCGGCTCGTATGTTGTGTGGAATTGTGANCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTA
CGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTCCAATCCCCCTGCCCTGATACGCGTCGGCAACCGTGAA
CGCGATCTCGGCGACCGTTCGGATCGGTTTCATCCCGCACAAAACGCGCGTCCGGTACGGGGTTCGCTTCGGTTCGTCAC
CACCCAGACGAAGTGGTCGACGTAGTCGACTTCCGACAGGTAGTGCATCAACGCCGGACTGGGAACACNAGCCGACAT
GAACCGTCGATACAGCGTCTCNCGGAGAAGTGGATGTGTCCGTGCACGGTCCGCTCGCGGTACCGGGCAGCACGGG
GCGTAACATCAGTTGAGTCCGCTCGGCAAGCCGTACCGGAATCGGGGAGACGA (SEQ ID NO. 373)

.....Rv2T7.seq.....
CAAGATGATCGCCGGTGCCACCCGATCCGTGCTCGGTTCAGCGCGAACGTGCTTTCGGTTCGGGCGACCACCATGTC
GCACGCACCGACCGAGGCCGAACCCGCCGGCCGCATGCCCGTTGATGGCGCCGACCACCGGCGAGCGGCGACTCGAC
GATGGCGCGCAACAGCGCCGTCAATTCGCGCGCCCGCGCCACCGCCATCCGGTACGGATCACCACCACCGCCGGC
CTCGCTGAGGTCCGCGCCGGCGCAGAACGTTCCGCCGGTATGCCCGAGCACGACCGCCGACCGCGGATCTGCTTC
GGCCGCACTCAGCCCTTGATGTAGTTGGGTGACCAGCGTGCTCGACAGCGCGTTGCGGTTGTGCGGAGAGTTAGTGT
CAGCCTGGCGAAGGGGCCGCCGAGGCGGGGCCAGCGTAGTCGACGGGGCTG (SEQ ID NO. 374)

Clone Rv301

.....Rv301SP6.seq.....
CTCAAGCTTCGATCGACAGTACTCCCGCCTTGGGTCTGGTCTTCGAGCTGGTTCGGTCATGGTTCGGACCTGCTGGTAGT
GGGGATCTAACGCAACATGGTTCGGGATTCATCATGGTGTACCCGTGATACCCATTTCGAGCTGCGGGTGAACCCCCGC
GATGCCGGGATTTCCAGCCGCACTAGGATGTCTAGCCGGCCAGCCGTGCCGCCGGACTTCGGGATGTTCCGGTATACC
ACCGATCGGCAATCTTGCNTATCCGCCGATGCTCGAACGCTAGCCACCCCAAACCAACCACTGTGACNACAATC

.....Rv301T7.seq.....
TGAATTTCCCGATCCCAATCTCGGTTTCAGATACAGGTGCGCCATACCCCTTACTTCGGCAACGCTGGGCGGATTGGC
CCTGCCGCTGCAGCAGACCATCGACGCCATCGAATTGCCGGCAATCTCGTTTCAGCCAATCCATACCCATCGACATTCC
GCCGATCGACATCCCGGCCCTCCACTATCAACGGAATTTTCATGTGTCGGAGGTCGTGCCGATCGATGTGTCCGTGACAT
TCCGG (SEQ ID NO. 376)

Clone Rv302

.....Rv302SP6.seq:.....
TACTCAAGCTTGAACGCTGCGAGCGAGCCCATGTAGAGCGTTTGGTACCAAACCGATCGGTGGGCCAACTTGCCATGG
GCTCACAGCGGCTATCGCGAGCGGTAGCCGATCATCGGCCAGGCGACGGTGGCCTGAGCGGCAGGGGTTGCCCTTATC
CATCCTCTTGCGGCATGGTTGCCGAGGGAGTGCCGGTAAGTCTGGTTCGGCAACCTGGCCCGCTGCGGGTTGGGTTTCG
GATTCCCTCGGCTAGTAAGGTGCTCGCCTGGTGTACAAACGAATCGCTAGAGAGCTCTTATCGGGAGTGGCCGTCGCG
ATCGTTGCGCTGCCGCTGGCGATCGCGTTCCGNCNTTACCGCCACCGGAACGTCCCAAGGTGCGCTCATCGGGCTCTAC
GGCGCCATCTTCCGCGGATTCTTCCNGCCGTGTTCCGGTG (SEQ ID NO. 377)

.....Rv302T7.seq:.....
GCGGTGTCTGAACCTTCCGCGTTCCCTCCAGCGCATTGAGCTTCAGCCCGACCGGCAGGTAGGGAGTCCGGCATGCGGT
CCTTCGCCCCGACCCCGCTGGCTAAATAGCCACCCCGAGCGCGGTACGGTCTTTGCACCGGGACGACGGCATACCG
GCAGCGCGAACATCGCCGCGGGCTGCAGCGTGAACGTGCAATACGAGTGAACAGTGTGCGCGCTAAAAACCCGAGC
CGGCGGTGCTTCGGTAATCAACGGCTCCTGCGCAACCAGCTGCAANTCNCGGTGCCACCGGCGTTGACAATCTTGA
TNTCGGCGACCTCGCGCACCAN (SEQ ID NO. 378)

Clone Rv303

.....Rv303SP6.seq:.....
TACTCAGCTTCGGCTCAGGTGGTGTGCTGGTAAAGTTCNCTGAACGGTGCAGGTTTCGACAATGTGGTGCCGGTTTCG
GCGGGTACTGCCATCGAGACACTGGCGCAGGCTATCGCACCCGTTATCGGCTACAAACAAATCGCGGTATGCGTTCTT
GAGCATGAGTCGGCGACCGTCTGTCATGGTCGACACCCACGACGGAAGACGCAGATCGCCGTCAAGCNTGTGTGCCGC
GGATTATCAGGACTGACCTCCTGGCTGACCGGCTGTTTGGTCNCGATGCCGCGCCCGGCGGCGT

.....Rv303T7.seq:..... (SEQ ID NO. 379)
CATCACCTGGTTCATGAACTGGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCAACATGAGCCAGCCTCTCGTCGGCGG
TCGGGTGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCCTGAAACCAGCTTCCATATCCCGCGACGAACG
ACGCCAGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACANCGCGTTCTCCACCGACCGGCGCGGGTGTGG
GGTGT (SEQ ID NO. 380)

Clone Rv304

.....Rv304SP6.seq:.....
CTCAAGCTTCCCGGCGGCCAGTACCGAAAGCGCGAAGCAGCTCGCGGCAGCCCAACNTGCTGCGTCGGATTGCCGGC
GGCGANATCAATTCCAGGCAGCTCCCGGACAATGCGGCTCTGCTGGCCGCAACGAAGGACTCGAGGTACCCCGGTG
CCCGGGGTCGTGGTGCACCTGCCGATCGCACAGGTTGGCCACAACCGGCGCTTGATGCCCGGTCGGCAAGCCCGGC
AGTTGCCAAACCCAGCGTATCAGGCTCGGCTCGCGAGTTTCGGCGAAGAAGTGGCTCGCCTGATCACCTACCATCGGC
CAGGATCTGCGTGTATCACNACGCTCGCAAGGAGGTTGTTGTGGTGCT (SEQ ID NO. 381)

.....Rv304T7.seq:.....
GCCACGTTTCGCGCGCGCCCGCATACGGCGGCGTACCGATCTCCGCTCATACACCCGCGGGTAATCGCCGACGGTGC
CGGTTTCGCGAGCCGAAGGTGACGACGCTGATTGAATCGAGTTCCAGGTCCAGCGGGTGGCGCAGCAACGGCGCGAGCT
CAACGACGTCAATCAGTTGTGCTTTCTACGGTCAACGACCCGGTGACCGTAGTCGCCCCGGTGCCTCGGCCGAGAA
GTTGCACCGCCACCAACCGGACACCGTCTTGACGCGGACGCCACCCCGGATCGGTTGTTGGCCAAGGTAATTGGGT
CATTCCATTGACGGGACGCCGACCCCGCAGCCCCAGTACCGCCACGACCAGCCGGCTGACCCCACTGTACGA
ACACCAAGGCGACGCCGACCA (SEQ ID NO. 382)

Clone Rv306

.....Rv306SP6.seq:.....
CTCAAGCTTGTATGCCGCTAAACCGAAGCGTGAGCAGCGCCGCCACCCACCGCGGGTTCGGGCGCCGGGCCCCGGGC
CGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCGAACCACCCGGCTGCGCTACGTCAAGCCATACCGGGCGGA
GCTACATCGGCTCGGCCGCCAGTGTTCGGGCCCTCTTTCGAGGTCNAGGTCNATACCGATTGCGCATCCCGAGCCG
CACCCTGGACGACAGAACCGTGCCCTACGAGTGCTTGTGCGGCGGGGCCAAAGAACANCTTGGCATCTTGGCGCGATT
GGCCGCGCGGTCTGCTG (SEQ ID NO. 383)

.....Rv306T7.seq:.....
CTCGGTACGCTTCGGTTCGAGTGTCGAGTGATAGATGACGACCGGGACCTCGTTCGGCATCTTCCATAGCCCGCCAC
ACCTTCAGTTGCTCACCGGAATCCAACCGGTANAANGTCGGCGAGCGCTCGGCATTGGTCATCGGGATATGCCGCTCG
GGACGCTCAGAGCCCTCGGGTCCGCCAGCACTCCGAGGCTTCGTGCGGGTGGTTCGCGACNCGCATGGGCCACCATC
GCATTACACAGGTCTGCGCG (SEQ ID NO. 384)

Clone Rv307

.....Rv307SP6.seq:.....
CTCAAGCTTCAATTCCTCCACGACGCGTTCCCAAATGAATTTCCCGATCCCACAATCTCGGTTAGATACAGGTCGCC
ATACCCCTTACTTCGGCAACGCTGGGCGGATTGGCCCTGCCGCTGCAGCAAACCATCGACGCCATCGAATTGCCGGCA
ATCTCGTTACGCCAATCCATACCCATCGACATTCCGCCGATCGACATCCCGCCTCCACTATCAACGGAATTTTCGATG
TCGGAGGTCGTGCCGATCGATNTNTCCGTCNACATTCCGGNGGTACCATCACCGGCACCAAGNATCGACCCGATTCCG
CTGAATTCGACGTTCTCAGCAGCGCCGAACCA (SEQ ID NO. 385)

.....Rv307T7.seq:.....
TTAACCCCGTGGCCTCTACGCCGCTNCGGGTCGAACATGCATCCCGAGCANATGCTCGAGCGCGCACCCACTCGC
CGATGGCCGGAACCGGCTGGTTACCCGGGTGGCGGCTGACGTTCCGGCGGCGAGGACATCGGCTGGGAAGGGGCGCTTG
CCACCGTCGTGAAGACCCAGATTGAAGGTGTTCTGCTGCTCTACGACATGACCCCGGCGGACGAGAAGAACCTTG
ACCGGTGGGAAGGCTCCGAGTTCGGCATCCACCANAAGATCCGATGCCGCGTT (SEQ ID NO. 386)

Clone Rv308

.....Rv308SP6.seq:.....
CTCAAGCTTGATTTTGATCATCATGGATGATCATACCCGAAGTGTGGTAGCCGAGTGGTTATCGTGGGTACCGTCG
TGCTTTCCATGGGCGCCTCTTTCGGGCTTTCGTTATGGTCTGGCAGGACATTCTGGGTATCGAGTTGTACTGGATGG
TGTTGGCGATGTCGGTGATCCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCCGGTTGAAAAANG
AAATTGGGGCCGATTGAACACCCGAATTATCCGTGCCATGGCTGGTACCGGGGGAGTGGTGACGGCTGCCGGCATGG
TGTTCCCGGTTACCATGTCGTTGTTGTGTTAGCGATTGCGAATTATTGGTCAGT (SEQ ID NO. 387)

.....Rv308T7.seq:.....
CGNCCAACCCGAATTGGTTTTTCGGCGCCNTCGGTGAGGACGGCGTGCGGGTGCTCAACGACGACGTCGTCCGCGGGAC
ACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGTACAACGCCGCGCGGAACGCTTCCG
CCNCGGCGTTACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATCGCCACCGGAGCGACGGC
CAAGGCGGCGTGCCAGGTGCCCCGGGCGCACGGTGCGGACAAGGTGGTGCTGGCGGTCCCGATCGGCCCANACGACAT
CGTGGCGAGATTGCGCGG (SEQ ID NO. 388)

Clone Rv309

.....Rv309SP6.seq:.....
CGTGACTGCCACCGGGGCCACTCCGCAGAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCGCCGA
CTTTCGCGGTAACCGCTCAACTTTGTGTCNACCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAATACTT
CATCCTGACGCCGGAACAAATTGACNCAGCGGTTCCNCTGACCAATACGGTCGGTCCCACGATGACCCANTACTACNT
CATTGCGACGGANAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCACTGGCGAACCTGGT
TCAACCAAACCTTGAAGGTGATTGTTAACCTGGGG (SEQ ID NO. 389)

.....Rv309T7.seq:.....
TCGCTCAAGCGCNTGAGGCCGAANCGGCTGGTTACGACTCCCTGTTTGTGATGGACCACTTCTACCAACTGCCCATGT
TGGGGACGCCCCGACCGATGCTGGAGGCTACACGGCCCTTGGTGCGCTGGCCACGGCGACCGAGCGGCTGCAAC
TGGGCGCGTTGGTGACCGGCAATACCTACCGCAGCCGACCTGCTGGCAAAGATCATCACCACGCTCGACGTGGTTA
GCGCCGGTCGAGCGATCCTCGGCATTGGAGCCGGTTGGTTGAGCTGGAACACCGCCAGCTCGGCTTCGAGTTTCGGCA
CTTTTCAGTGACCGGTTCAACCGGCTCGAAAAGGCGCTACANAT (SEQ ID NO. 390)

Clone Rv30

.....Rv30SP6.seq:.....
ATACTCAAGCTTCCGCTGGGGCCTGTCAACCATGGCGATCCCGTTGGTCCCGGACATCCCGAACGAGGACACCGCGA
CCCNCTTCGGTGTGTGATCATTACCGTTGGGCCACTGCGTAACCGCTTGCGGCACAAAGAGCCCGGTCTCGACGTCCG
AAAGCTCATCGGGCACCCGATTGAAATGCAGCAGCGGCGGCCACACCCCGTGCCGAGTGACAGAATTGCCTTGATCA
GCCCCAGGTCGCCGCGGATGCCGTGCTGTGCCCCATGTTGCTCTTGGCCGATCCAAGCGCGCAGGGGGTGCCCCGCGC
CATAACCCGCGCCAGGCTGCGGTACTCAATCGGGTCGCCGATTGGCGTACCGGTGCCGTGCGCCTCCACCACACCGA
CCGTTTCGGGCTG (SEQ ID NO. 391)

.....Rv30T7PEG.seq:.....
CAACAGCGTTCCAGCGGCATACACCGCACATGCCGTGCACCCGGCGCGGGCGGAGTCGCCGATAACACANGTACA
CCTTGGGAATCGGTGTGCGCCAGGGATTNACCGCGGGGTGGGGCCGGCGATCGCGCGCCAGGTTCGAGTTGGCGCCGA
CCGTGATNTACCGCCGACGTAGTTGGCGTTGTGGTCCGCCATCCGCGCGGCGGGCACGGCGCGGGCCGCCACCGA
TGTCACGGAAGCCGGGGGCGAACGCTCGACGACCTGGTTACCGTCTCNGTCGNTCNANCGTGGACCCGACNGCACGT

GGGCATATGTCCANAACGGACGNGGCCGGTTTCNTCGATGCNGCCGGGGTCCGCGACNTGCGGACNCNCNGNCACACC
ATCCGCCAGTCCGCGTGGCGTCCGCCCGGACTCTGCCTCGGCCCGGCCA (SEQ ID NO. 392)

Clone Rv310

:Rv310SP6.seq:::

CTCAAGCTTTGNCGACGATCGGGCGATGTCGATGANAGGAAACCCAGCGCACAAACCGACNATTTTGGCGTAGCCGGC
GGACNTCTGCTCGATTCCGATCACGTGGCGCTCGCATCGAGCATGGCGCCGGCGACGGCTAGCAGCGATCCGCCGTC
GTCGAGGAACACGACACGAGCCGTACGCCCGGCCGTAAGCCGCGCCAGGATTCGGCGAAAAACCGTTCTACGTGGCG
GGTGTACTGGGTGTCAATGATTCTGTGGGTGCGTAGGCGTCTGCAATCTGCGACATAAATGCCGTCCGCCCGCAT
CCGCTCAACAACCTCCCGGGTGGTGAATANCACTTGCCGA (SEQ ID NO. 393)

:Rv310T7.seq:::

TCCAACGCGGTGACAGATTGTCTATCCTGGACCTGACGGTGAGGTGGAAGTTTCCAGGAATTCGGCAAAATCGGTA
AGAGCCTGAAGAATTCGGTATCGCCGGACGAAATCTGCGACGCATACGGGGCAGATACGCTTCGGGTTTACGAGATGT
CGATGGGGCCGCTGGAGGCTTCACTCCATGGGCCACAAAGGATGTTGTGGCGCGTACCGTTTCTGCGAGCGGGTGT
GGCGCTTGGTCTGCGACGAGCACACCGGCCGAAACTCGGGTGGCTGACGGCGTGGAATCGACATCGATACGCTACGGG
CGTTGCACCGCACCATCGTCGGCGTGTC (SEQ ID NO. 394)

Clone Rv311

:Rv311SP6.seq:::

CTCGTCCTTGACTACGCCAGTATCGAAANCCTCCTGTGCCGGTNCGCTAAACACCCGGCGGACACTCANACGGTGCT
GGTGGTGCGGCATGGCACCGCGGGCAGCAAAGCGCACTTCTCCGGGGACGACAGCAAGCGACCGCTAGACAAGAGGGG
TCGTGCGCAGGCAGAAGCGTTGGTACCACAGCTGCTGGCGTTCCGGCGCCACCGATGTTTATGCCCGCGACCGGGTGCG
CTGCCACCANACNATGGAGCCACTCGCCGCGGAACTGAACGTGACCATACACAACGAGCCNCCCTGACCGAAGAGTC
CTACGCCAACACCCCAACGCGGCCGACACCGAGTGCTGCAGATCTTCG (SEQ ID NO. 395)

:Rv311T7.seq:::

GTATCGCCTCCNCCCTTGGCCACCAGCAGCCACAGCGCGGTTCCGCGACCGAACGTGGACATCAATAGCCCGGAATCG
GTGTGTGCAAGTTGGTAAACGGTGTTGATCCCAAGCTTTGCCAGCCTTTTCGTAGTCTTGGGCCCCACACCCACAGT
GCTTCGACGGTACGGTACCCATGATGGCCATCCAGTTGGCATCGGTGAGCTGATAGATGCCAGCTGGTTTCGCCAAC
CCGGTAGCGATCTTGGCGCGCTGCTTGTGTCACCTGATACCTATCGAGCAAGACAGCCCGGTTTGGGACAAGATGACT
TTTCGGATCTCTTCNGCGAACTTCCAATGGGGGTCTCCGGGANT (SEQ ID NO. 396)

Clone Rv312

:Rv312SP6.seq:::

CTCAAGCTTTTGGTCTAGCCGGCCGAGCACGATACGGGTGTCCTTGCCACCGGCGGGCGGCTGTCCGGGAAATGGCGG
GTCCCCGGTGTTTGTGTGANGANTGCTGAACCGTAGTCAAGTGGGCGCGCTCAGACTCCACCCAGCCAGCAGGCAG
CGCGAAGCTGAATCTCCAACCGGGTGTGCGATCCGGACAGGTTGGGGTGGCTTGGGGCAATGACAGGTGGCGGCGG
TGCGTTCCGGTCCGGCCGGCGGAGGTGCTGCGTTGGGATCNCCTGGCTGGGCATTCCGCNTNTTGGCGGCGGCGGTGG
TGGGGGGGCAACANGTGTCCCGGTGCGGTGGCGCTGC (SEQ ID NO. 397)

:Rv312T7.seq:::

ATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCCCGACTTTCGCGGTACCCGCTCAACTTTGTGT
CGACCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAATACTTCATCCTGACGCCGGAACAAATTGACGCAG
CGGTTCCGCTGACCAATACGGTCCGTCCACGATGACCCAGTACTACATCATTGCGACGGAGAACCTGCCGCTGCTAG
AGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGTTCAACCAAATTGAAGGTGATTGTTAACC
TGGGCTACGGCGACCCGGCCTATGGTTATTCGACCTCGCCGCC (SEQ ID NO. 398)

Clone Rv313

:Rv313SP6.seq:::

CTCAAGCTTGCAATGCGGGTCCGGATGCCATGGTTGGAANATGGTCCGCTGCGCTCNAATACGCGCGAGCGCATGA
GCTCACCGGTTCCGAACAACGTATCGAAAAACGTGCGACTGCTGGCAGATGGTATCTCCGATGTGGTTGTAATTTGTA
TCCCAACTCTAATGTGCTATCGGATCAGCGTGAATATCGANATATTGCGAATGCGATGACAGGCCGCCATTCCGGTTT
ATTGCTTACGCTTCCCGGGTTCGATTCGTCTGATGCACTGCCGCAAAACGCGGATATGATTGTTGAAACCGTATCTA
ACGCAATTATTGATGTGGTAGGCGGCAGCTGCCGTTTTGTGCTGTCGG (SEQ ID NO. 399)

:::Rv313T7.seq:::

CAAATACACGCCGGACGCACAGCGGACATCGCCATCCCGAGCACACCCAAAACGGGATACAGGATGGAGGCCAACGC
CACGGCCGCGCCAGGATCACCAACCACACCGGCTTGGTCAGCTTGTGCGCGGGTATAGGCATCGGGCCGCTGCAA
CGCAGCATGCACAAACGCGTACACCGCTGTACCAAGACGGCGACCAGCAATACCAGCATGACGGTACCCACGAGGTG
GCTCACGCATTACAGACTATGCGGTTTGCATCCAACACG (SEQ ID NO. 400)

Clone Rv314

:::Rv314SP6.seq:::

CTCGTCCTTCGGCCTCGCTGCAGGAGTGGGAGCCGACGGGCTGGAAATCCGAAAAACGAGCCGGTGATCGCACTGTGCG
CCGATCGGCGCGCCACCTGGTTGGTGTACGGATGAATCCGCAGCGAAATGTGGCTGCGGTGGCGTGTCTGACTCGT
TGGCGTCGACGCTGGTGGCAGCCACCGAGCGGTGGTCCAGGATCTGGATGGGCAAGTTGTGCGGCCCGCGGTTGA
CGGCCGATGAGCTGACCGAGTGCAGACGCGCGTGTGGCTGACTTGAACCGACATGGAGTGCCTCCGGTT

(SEQ ID NO. 401)

:::Rv314T7.seq:::

GTCTAGNCCGCGAACACGATACGGGTGTCTTGGCCACCGGCGCGGCTGTCCGGGAAATGGCGGGTCCCGGGTGGT
TTTGTCTGAAGANTGCTGAACCGTAGTCGAAGTGGGCGGCGTCAGACTCCACCCAGCCAGGCGAGCGGAAGCTGAA
TCCTCCAACCGGTTGTGATCCGGACAGGTTGGGGTGCCTTGGGGCAATGACAGGTGGCGGCGGTGCGTTCGGGTC
GGCCGGCGGAAGTGTGCTGCGTTGGGATCGCCCGGCTGGGCATTGCGCGTGTGGCGGCGGCGGTTG

(SEQ ID NO. 402)

Clone Rv315

:::Rv315SP6.seq:::

ACTCAAGCTTGAGATTGGCGTCAACGGGTGTGCGCACCGGCGTCTGCAAGTTGGTAGGCCTGCAGTTTGTGCATCAGG
CCGATGCCGCGGCGCTCGTGGCCACGCATGTACANACCCACGCGCGCCCTCACGGGCGACCATCGCCAGCGCGGCG
TCCAGCTGAGGCCCCGAATCGCAGCGGCGTGACCCAAACACATCGCCGGTCAAGCACTCCGAATGCACCCGGACAGC
ACGTCG

TCACCGTCGGCGTTGGGCCCCGGCGATCTCGCCGCGGACCAGCGCGACATGTTCCACGTCCTCGTAAATGCTGGTGTAN
CCGATGGCGCGAAACTCCCCATGACAANTCGGAATCCCGCGCCTCGGCGACCCCGCTCAATGTTGCTTCTCNTGCTTG

(SEQ ID NO. 403)

:::Rv315T7.seq:::

TGCACNAGCATCTTGACNGTTGTTTTGGCTCGGCATGGTTAGCCAAGGTTCTGCGGTCCCACAGATCATCTTGGTC
CGGTAGCGCTCGTCCGGGTATGCTGCCGCGGGATTCTCGCTGCTATTACTCCCCCGAAGAACGCCACCGGTCCAGC
GCGTGGGCGCGCGGTTCCCATCACAACCTGAACCCCCAACAGGGGACATGCTTAGCGGTAGGGCGCGGCCAAGGC
GGCAGCAATCGCATCACTGCGCTGCGCGTCACTATTAACCCACCCGGACTTCACTTCCACGACCCGAATGGCGCCCCG
TGATTGATCATCTTGCGCACCGCGGATAATCCGGGAT

TG (SEQ ID NO. 404)

Clone Rv316

:::Rv316SP6.seq:::

ACCGGGGCCACTCCGCACAATCTGTACCCGACCAANATCTACACCATCGAATACGACGGCGTCCGCGACTTTCGCGG
TACCCGCTCAACTTTGTGTCNACCCTCAACGCCATTTGCCGGCACCTACTACGTGCACTCCAACCTACTTCTGACG
CCGGAACAAATTGACGCNCGGTTCCGCTGACCAATACGGTCCGTCCACNATGACCCANTACTACATCATTCGCACG
GANAACCTGCCGCTGCTAAAGCCACTGCGATCGGTGCCGATCGTGGGAACCCACTGGCGAACCTGGTTCAACCAAAC
TTGAAGGTNATTGTTNACCTGGGCTACGGCGANCCGGCCTNTGGTTATTCCACCTNCCGCCCAATGTTTGCNACTCC
CGTTCGGGGTTGTTCCCNNAAGGTCAACCC (SEQ ID NO. 405)

:::Rv316T7.seq:::

CGCTCAAGCGCNTGAGGCCGAANC GGCTGTTACGACTCCCTGTTTGTGATGGACCACTTCTACCAACTGCCCATGTT
GGGGACGCCCGACCGGATGCTGGAGGCCTACACGGCCCTTGGTGCCTGGCCACGGCGACCGAGCGGCTGCAACT
GGGCGCGTTGGTGACCGGCAATACCTACCGCAGCCCCGACCTGCTGGCAAAGATCATCACCAGCTCGACGTGGTTAG
CGCCGGTCGAGCGATCCTCGGCATTGGAGCCGGTTGGTTTGANCTGGAACACCGCCAGCTCGGCTTCGAGTTCGGCAC
TTTCAGTGACCGGTTT (SEQ ID NO. 406)

Clone Rv317

:::Rv317SP6.seq:::

CTCAAGCTTGCGTTCGATGAAGTAGTCGTGCGTCAGCGCCGCCTCTTCGAGCTCCTTGGCGATGCCAGCAAGGAGTC
ATCGCCGCGAGCTTGGCCAGGATCTTGTGCGCCTGTTCTTGACGATGCGGGCCCGCGGATCGTAGTTCTTGTAGAC
ACGATGACCGAAACCATCAATTTGACCCCGGCTCGCGGTTCTTGACCTTGCCTACAACTCGCTGACGTGCTGCGC

GCTGTGCGGAATGCCCTCGAGCATCTCCAGGACAGCCTGATTGGCGCCGCCATGAAGCGGACCCCATAGTGCGTTGATGCC (SEQ ID NO. 407)

.....Rv317T7.seq:.....
GGTCAGGCCGAGCAGGCGCGAGGAACGACGAACCAACAAGCCATGGTGGTTGGCGCCGTCGAGAGGTCGGCGGTCGC
CACAACGGGAAGATCGCCTTGAGCGTCGCTCGACCGCCGCCTCGAGTTGGGTCATAACGAAGTAGCTGATGCCGATCA
TGTCGACGTTTCCGTCGCATCAGCGTGCAGCGGCGACCCACTCNACGAGGTCTCGGTGCCGCGCGGCCAGGGCACCA
GCAGTGACGAGTCCAGGCGCCGTCGGGCCAAGCAGTCGCGGTGCCANCCGTGGTGGGTCGGGCGATGGTTGGGTGTGC
TCATTTCGGGAACGCCA (SEQ ID NO. 408)

Clone Rv318

.....Rv318SP6.seq:.....
CTCGAAGCTTTAACAGCATCAACCCCGCCCCGCCACGACCGACACNATGTCGATGCCATCGAGGTGAATGTCGAAC
TGCGCGAAACCATCGGCGACCGCGACCACCGGCAACATGGGTACCGGCGATTTCGGGTGCCAATGCCGACCCGACGGG
CCGCTCTCACCGCAGGTGACCTCGATCACCGAGACCANCCGGCCGTTTNTNTACGACCCCTACCGTGTACGCCCCA
AAACGGCGCTGGTGGTCGATTGCCGGAGTGCACCCCNACCCAGTGTGTCGCCGCGATCC (SEQ ID NO. 409)

.....Rv318T7.seq:.....
TGATGCCGCAACCGATCGACGGTCGTTGGTCGGGGTTGACTGGCCGCCCCGGCGAAGCAGGGCGTCGACCGCGGCCCGG
ACGTGCGCGCGCGCTCACCGGTCGGCCATTGCCCGGGCGGGAGTCGTCGAGCTGACCACGGTAGACAAGTCGGCGCTGG
CCGTCGAAGACNAACGTGTCGGGTGTGCAGGCCGCGGAGGAAGGCGCGGGCGACNTCTTGGGTTTCGTCGTANAGATAC
GGGAACGTCCAGCCGTGGCGGCGGGCCTCGGCGACCATCTGATCGGGCCCGTCC (SEQ ID NO. 410)

Clone Rv319

.....Rv319SP6.seq:.....
TTTCGGGCGAGGCGGTATANTTTCCNTCTGACCGGCGACCGCCAGCCGANAAGCTCGTTTTCCAGTGTTGCTGGGG
ATTCTCACGCTGCTGCTGANTGCGTGCCAAACCGCTTCCGCTTCGGGTACAAACGAGCCGCGGGGCTACNATCGTGCG
ACGCTGAAGTTGGTGTCTCCATGGACTTGGGGATGTGCCTGAACCGGTTACCTACNACTCCAAGCTGGCGCCGTCT
CGTCCGCAAGTCTGTGCTTGCGATAGCCGGGAGGCGCGGATCCGCAATGACGGATTCCNTGCCANCGCTCCGAGTTGC
NTGCGGATCGACTACNAATTGATCACCCANAACCATCGGGCGTNTTACTGCCTGAAGTACCTGGTGCGGGTCGGATAC
TGCTATCCGGCGGTGACAACCCCGGCAAGC (SEQ ID NO. 411)

.....Rv319T7.seq:.....
GTTTTGGCTCGGCATGGTTAGCCAAGGTTCTGCGGTCCCACAGATCATCTTGGTCCGGTAGCGCTCGTCCGGGTATG
CTGCCCGCGGGATTCTCGCTGCTATTACTCCCCCGAAGAACGCCACCGGTCCAGCGCGTGGGCCCGCGCGGTCCCCA
TCACAAACTGAACCCCCAACAGGGACATGCTTAGCGGTAGGGCGCGGCCAAGGCGGCAGCAATCGCATCACTGCGCT
GCGCGTCACTATTAACCCACCCGGAATCACTTCCACGACCCCGAATGGCGCCCGGTCAATTGATCATCTTGCGCACCG
CGGATAATCCGGGATTGCCAGCCATTCTACTACCGCATGCGAGTCATCGGCTGACCGCAGCGGTC

(SEQ ID NO. 412)

Clone Rv31

.....Rv31SP6.seq:.....
TCGCCTAGGCGGGCTTCCCCTTCCGTCCGAGCNGTCAGAAGCTCCTATGACAATGCACTACCCGAGACNATCAACGGC
CTATGCAATACCNAGCTGATCAAACCCGGCAAGCCCTGGCGGTCCATCGAGGATGTCGAGTTGGCCACCGCGCGCTGG
GTCGACTGGTTCAACCATCGCGCCCTTACCGGTACTGCGGCGACATCCCGCCGGTCTAATCGACGCCGCGCTCACTA
CGCTCAACGCCAGAGACCANCCGCGGTGACGTCTCAGATCAGAGAGTCTCCGGACTCACCGGGCGGTTTCATCCCC
ACTGTCGATAGCGTCTGTGGATAACTTTGTCTGCA (SEQ ID NO. 413)

.....Rv31T7.seq:.....
GCGCGTNGAACTGATAGGTGCGGCGCGGCTCGAGCANGCCGGCCATTTGTTGATGCGGTTACCGAAGATCTCTTCGG
TGACCTGCCCGCGCGCGGCGAGCTCGGCGCAGTGCCCGGCGTTGGCCGCCGCGGCGACAATCTTGCGTCCACGGTGG
TCTGGGTCA (SEQ ID NO. 414)

Clone Rv321

.....Rv321SP6.seq:.....
CTCAAGCTTCAATACAGAGTTATAAACTGTGATAATCAACCCTCATCAATGATGACNAACTAACCCCGATATCAGGT
CACATGACGAAGGGAAAGAGAAGGAAATCAACTGTGACAACTGCCCTCAAATTTGGCTTCTTAAAAATTACAGTTT
AAAAAGTATGAGAAAATCCATGCAGGCTGAAGGAAACAGCAATAACTGTGACAAATTACCCTCAGTAGGTGAGAACAA

ATGTGACGGAACCACTCTCAAATCTGTGACAGATAACCTCAGACTATCCTGTCGTCATGGAAGTGATATCGCGGAAGG
AAAAAT (SEQ ID NO. 415)

Clone Rv322

.....Rv322SP6.seq:.....
CTCAAGCTTCGATCGACATTACTCCCGCCTTGGGTCTGGTCTCCGAGCTGGTCGGTCATGGTCGGACCTGCTGGTAGT
GGGGATCTAACGCAACATGGTCGGGATTATCATGGTGTACCCGTGATACCCATTGCGAGCTGCCGGTGAAACCCCGC
GATGCCGGGATTTCCAGCCGCACTAGGATGTCTAGCCGGCCAGCCGCTGCCGCCGGAATTCCGGATGTTCCGGTATACC
ANCGATCGGCAATCTTGCGTATCCGCCGATGCTCGAACGCTANCCACGCCAAACCAACCACTGTGACNACAATCGCCA
CCACACCAAAGGTCATGCCCTCGGCGTGATGTCCGGTGCCGAAAGCCGCAAGAGCTCCGACGCCGCC

(SEQ ID NO. 416)

.....Rv322T7.seq:.....
CATTCCCAATTGAATTTCCCNATCCCAATCTCGGTTAGATACAGGTCGCCATACCCCTTACTTCGGCAACGCTGG
GCGGATTGGCCCTGCCGCTGACGACANACCATCGACGCCATCGAATTGCCGGCAATCTCGTTAGCCAATCCATACCCA
TCGACATTCCGCCGATCGACATCCCGGCCCTCCACTATCAACGGAATTTGATGTGCGGAGGTCGTGCCGATCGATGTGT
CCGTGACATTCCGGCGGTCACCATCACCGGCACCGAGGTCGACCCGATTCCGCTGAATTTCGACGTTCTCAGCAGCG
CCGGACCCATCAACATCTCGATCATCGACATTCGGGCGCTGCCGGGCTTTGGCAACTCGACCGAGCTGCCGTCGTCCG
GCTTCTTCAACACCGGCGGCGGTGGCGGCT (SEQ ID NO. 417)

Clone Rv327

.....Rv327SP6.seq:.....
CTCAAGCTTTTCGGCGGAGACGGACANNTTGCGAACATTGATGACAAAATAGAAATCATTGATGGTTTGAGTCACCAGG
CCGATCAAGCCTTCGCCGAGCCAAATCCAATCAAGAGGCCCAAGCCCGTACCAATCAGCCCGGCAACGAGGGATTCC
GTCATTATCAGCCAAAATAACTGCTCTCGGGTTACACCCAAACAGCGCAATATGGCGAAAAACGGTCGCCGTTGCACG
ACATTAAATGTCACGGTATTG (SEQ ID NO. 418)

.....Rv327T7.seq:.....
AGCTTAACTGCTCCCTAATACTGGGGCTGTGCTGCGGTGTATGCACGGCATAACGGACATCCNTCCCCTGAGACCCN
CGGTCTAATCAGCCACGTGTCCACCATCAGGGGTCAACCCCGGCCAAGGGCGACGGCACCCCAAGTTCCGCCACCGTT
AACCTATTGCTGTGAGCTTCATTTGCTGCGAGCAAAACAGTTGGTCGGCCGTTAGGAACTGAATTGACACTCAACCGA
TTTGGTGCCNCCGTAGGTGTCTGGCTGCGGGTGCGTGGTGTGTCGCGTGTGGTAACGACCACAATGTGACCGGG
GGAGGTGCAACCACTGGCCACGCGTCCGCGAATGTCTATTGCGGGGG (SEQ ID NO. 419)

Clone Rv328

.....Rv328SP6.seq:.....
CTCAAGCTTGGGGTGGCGCTGTGCGTGGTGTGCTTGGCGGCGTGGTATCAACACCGCCACGAAATGGGGCACAAG
AAGGATTGCGTGGAGCGGTGGCTGTCCAAAATCACCTCGCCCCAGACCTGCTACGGGCACTTCTACATCGAGCACAAC
CGTGGCCATCACGTCCGGGTGTCCACACCGGAGGACCCGGCGTCCGGCGGGTTCGGCGAAACGTTGTGGGAGTTCTTG
CCCCGAGTGTATCGGCGGCTTGCCTCGGCCGTTTATTGGAGGCCAACGGCTGCGTCCGGCTCGGCGTCAGCCCC
CT (SEQ ID NO. 420)

.....Rv328T7.seq:.....
GCACCAAGGCCCCACACGTCAACCTGTGACCTCCTGCGCCGACCCCGCCGAGGTCCTGGCCGTTACCACCTGAACGG
GCGAGCCGGGAGTCTGGTACGCATCGAACAAAGAGCAAGGTGCATGGGCGGAGTTGTTCCGCCACTTCGTGATGACG
GGGTCNATCCATTGAGGTCCGTGCGCGGTCGGTCGAGTGGCGGTCACACTCCAGGTACTCGACCTCACAGACGAGA
GGACTCGATCCCATCTAGGTGTGGACGAAACAGATCTTCTGTCCGA (SEQ ID NO. 421)

Clone Rv329

.....Rv329SP6.seq:.....
TCGCCTCCGCATATGGGTCGACGCCAAGCGGGTCCGGATTTCTGGGCTTCATCGCTCGCGCCGTCGCGACAAACAGCG
CGTCCGAACCGACACTCGTTGTGATGTCCAGCTATCACCTTCGGTACGCACCCAATCGACCTACNCGGCTATCTCA
GCCGCGATCTCCAGGTCCGCGGAGCCAGGTGCATCCCGGTCCGGATCCCACTAACCCGGCACCAATTGGCGTCN

(SEQ ID NO. 422)

.....Rv329T7.seq:.....
GTCCTCGAGTGCCGCCGTCGNACNCCCAGCGCCCGCGCGGCCACTTGGATGCGACCCGTTTCAAGTCCCTTCATCAT
CTGCGAAAAGCCTTGACCATGGCTCCGCCCAGGATCGCCGAGACCGGCACCCGGAGGTTGTCGAACGACAGCTCGCA
GGATTGACGCCCCCTGTAACCCAACTTCGGCAAGTCCCGGACACCGTGAGTCCGGGCCCGGGTTCGACGAGCACGAT
CGACATGCCTTGGTGCCGCGGTGTGGCGTTTCGGGTCGG (SEQ ID NO. 423)

Clone Rv32

.....Rv32SP6.seq:.....
GGCATACCAATGTGGACTTCTGCTCACCACGATATCCGTGGTCTGATCCGCTGCTGCGGCGGGGCTGCNACCTGCNTC
TCNGCGGCACCCGCTNACTACATGGCNCGCGCCGACGACATACGTCGCGGCGGGGACCCACTCCNACTGGTCGACGGTGC
TGGCCGCGTGTCCGCANGTCCCNAACCCGCGCCGACCGACGAAACCGGCGCGCTCCGTCTGGACCAACGCTCATGT
GCCGTGCGGGTCCATGCTCGACGCCATCGAGACCGTAACCAGCGTCCTCGAGCGGTTCGCCTCCGGCTCCGTGACAT
CTTCGTGGTGTGCTCGCGCGGTGCCGCCGCGCGGATGGTCGACCACAACGCCAACCACTCGGCGGTGACATCACCGTC
CGCGCCACTCGACCTGGCGCGCATCGCGGCC (SEQ ID NO. 424)

.....Rv32T7.seq:.....
GTGAGCAGACCTACGCCNCTGGTTGCGCCAACCTCGGTACCGATCATGGCGCGCNGCCTGTCTGTCACCGATACCCAGC
GAACAAGACAGCCCGGTCCGCGACAAGATGACTTTCGCGACTTCCATGGGGTCTCCGGAGTCCCG
GGCGCCACCGCGAGGTAACCTCGTCTCAGTCCCATACGCGACCGGGTATCCACGTGCGCGAACAACGCCACCACTC
CCCAGACGCCNCGTTGTACGCGGTGGGTTCACNGCAATAAGTGGCTCANGGCATCGTCCGGCGCGGTCCNCAAC
GCA (SEQ ID NO. 425)

Clone Rv330

.....Rv330SP6.seq:.....
CTCAAGCTTGAGGTTAACTTTGAACGGATCGAGCTGGACGTTTCGAGACGGTGATCGGGCCGAACCTGAATTGTCCGGT
AATGCCAACGCAAAAAGCAGGTGGTGGCCGGGGCGGTGAAACCGGCTCGGCGGCACCGTCGAAATCTATGTGGAT
TGCCGGAATGGGGATGTCCGGCACGGCGAAACCGTAGTTCGCTTGTCCCGTGAGGCCCAGGTGGATGGGGGAAAGAT
CCTGGTGTCCGGGATAATAATGGGGCCGATGCCCGCGTTGAAGTCCACTGGATCGGGAATCCGGAATCTTGATCCG
ACGTTACAGCCGAACAGGCCCTC (SEQ ID NO. 426)

.....Rv330T7.seq:.....
CGGCGACGTGCGGATACGCCGAGCAGTTGGGAATCGCTCTGCAGCAAACCAATATTCTGCGCGACGTTTCGAGAGGACT
TTTTGAATGGACGGATCTACCTGCCGCGGACGAGCTGGACCGATTAGGCGTACGCCTCCGCTGGACGACACCGGGG
CACTCGATGACCCCGACGGACGGCTCGCGGCNCTGCTGCGGTTCACTGCCGACCGCGCCGAGACTGGTNTTCGCTGG
GACTGCGGCTGATTCCACACCTCGACCGCGCAGCGCTGCCTGCTGTGCGGCCATGTCTGGCATCTACCGCGCTCAGC
TCGCCTTGATCAGAGCATCGCCGGCGGTCTGCTA (SEQ ID NO. 427)

Clone Rv331

.....Rv331SP6.seq:.....
CTATAAAATACTCAAGCTTGATGCCGCCGAACCCGAGCGTGAGCACGCCGCCAGCCACCACGCGCGGGTCGGGCGCCG
GGCCCGGGCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACCACCGGNTGCGCTACGTCNAGCCATA
CCGGGCGGAGCTACATCGGCTCGGCCGCCAGTGTTCGGGCCCTTTTCGAGGTCNAGGTCNATACCGATTGCGCAT
CCGACGCCGACCCCTGAACNACANAACCGTGCCCTACTATTGCTTGTGNGCGGGGCCAAAAACAGCTTGCCATCCT
GGCCNATTGGCCGGCGCGG (SEQ ID NO. 428)

.....Rv331T7.seq:.....
CTTCGTGCGAGTGTGCGAGTGATAGATGACGACCGGGACCTCGTCGGCATCTTCCATAGCCCGCCACACCTTCAGTT
GCTCACCGGAATCCAACCGGTAGAAGGTGCGCGAGCGCTCGGCATTGGTCATCGGGATATGCCGCTCGGGACGGTCAG
AGCCCTCGGGTCCGGCCAGCACTCCGCAGGCTTCGTGCGGGTGGTCGCGACGCGCATGGGCCACCATCGCATTACCA
GGTCTGCGCGAATCNCCANCACGTANACNGTTCCTTTCTAA (SEQ ID NO. 429)

Clone Rv333

.....Rv333SP6.seq:.....
CTGGCACCAAGGCCCCACACGTCACCCTGTGACCTCCTGCGCCGACCCCGCCGAGGTCTTGCCGTTACCAACCGAAC
GGGCGAGCCGGGAGTCTGGTNCGCATCGAACAAANAGCAAGGTGCATGGGCGGAGTTGTTCGCCACTTCGTGATGA
CGGGTCNATCCATTGAGGTCCGTGCGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT
AAGGACTCNATCCCATCTAGGTGTGGACNAAACAGATCTTCTGTCGACNACTACACCACCAACCCAGGCCATCGCCGC
CGCCCGGATGCCAACTTCGACGCGGTACTGGCCCGGCGGGGGCGCTCCCGGTTGTCAACACTTGCCGTGTTCTNT
TCACGCNCTGCCCCACATCCAACCCAACG (SEQ ID NO. 430)

Clone Rv334

.....Rv334T7.seq:.....
GTTCTTGGGCCCCATGCGGAGGTATCGCCGTTTCCACCACGCGGTGCGGGTGGCGTTGCATTAGCTCACCGATGGTGCG
CTTGTGAGGCGCGGGGATACCCGAGTGCCGGTAAACCATCTTGCTGCTG (SEQ ID NO. 431)

Clone Rv335

:::Rv335SP6.seq:::

CAATACTCAAGCTTGGCGTGCCGTTCCAACCGAATTGGCTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTCA
ACNACNACGTCGTCGCGGGGACACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTAC
AACGCCGCGCGGAACGCTTCGCGCGGGCGTGACCGCATCCCCTTGACCGGGCGGATC (SEQ ID NO. 432)

:::Rv335T7.seq:::

CNTCATGATGATCATCACCGAAGTGTGGTAGCCGAGTGGTTATCGTGGGTACCGTCGTGCTTTCATGGGCGCCTC
TTTCGGGCTTTCGCTATTGGTCTGGCAGGACATTCTGGGTATCGAGTTGTACTGGATGGTGTGGCGATGTCGGTGAT
CCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCCGGTTGAAAGAGGAAATTGGGGCCGATTGAA
CACCGGAATTATCCGTGCCATGGCTGGTACCGGGGAGTGGTGACGGCTGCCGGCATGGTGTTCGCCGTTACCATGTC
GTTGTTTGTGTTACGCGATTTGCGAATTATTGGTCAGATCGGTACCAC (SEQ ID NO. 433)

Clone Rv336

:::Rv336SP6.seq:::

ATACTCAAGCTTTACGGTGATCGNCATCACCTGGTTCATGAACTGGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCA
ACATGAGCCAGCCTCTCGTCGGCGGTGCGGGTGCAGGTGCTCGGGCAGCTCGGCCGNACAGCCGCTGACCTGAAAC
CAGCTTCCATATCCCGCGANNAACGACGCCAGTCCGCTACGTNACCCCTCCGCGACTGTCCATGGACAACAGCGCGTT
CTCCACCGACCGGGCCCGGTGTGGGGTNTT (SEQ ID NO. 434)

:::Rv336T7.seq:::

GCTGGTAGAGTCGCTGACCGGTGCAGGTTTCGACAATGTGGTGCCGGTTCGGCGGCTACGTGCCATCGAGACACTGGC
GCAGGCTATCGCACCCGTTATCGGCTACGAGCAATCGCGGTATGCGTTCCTTGAGCATGAGTCGGCGACCGTCGTAT
GGTCGACACCCACGACGGAAGACGCGAGATCGCCGTCGAAGCATGTGTGCCGCGGATTATCAGGACTGACCTCCTGGCT
GACCGGCATGTTTGGTCGCGATGCCTGGCG (SEQ ID NO. 435)

Clone Rv337

:::Rv337SP6.seq:::

GCTTTCGCGGATACCCGCCATGTCNCGCACATCCAGGACTTCTGGGGGGATCCGCTGACAGCGGCGGGATCCCAAAG
TCCGGATGATCGGGCCGCTACGTCGTGGTGTACCTCGTCGGTAACAACGAAACCGAAGCGTATGACTCGGTCCACGC
GGTGCGGCACATGGTGGACACACCGCCACCGCACGGGGTGAAGGCCATATGTACCGGTCGCGCANCACTCAATGC
CGACCAGGCCGAGGCCGANACAAAANTATCGCTAAGGTCACCGCATCACNAGCATGGTGATCGCAGCAATGTTGCT
AGTGATCTATCGCTCCGTAATTA (SEQ ID NO. 436)

:::Rv337T7.seq:::

CTTCCAACCCGAATTGGCTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTCAACGACGACGTCGTCCGCGGGAC
ACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGCTTCCG
CCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGCGCATCGCCACCGGAGCGAGGGC
CAAGGCGGCGTGCCANGTCGCCCCGGCGCACGGTGCGGACAAGGTGGTGCTGGCGGTCCCGATCGGCCCA

(SEQ ID NO. 437)

Clone Rv338

:::Rv338SP6.seq:::

TACTCAAGCTTCGCGAGATCCGGATGGCACTCACGCTGGACAAGACCTTCACAAAATCTGAAATCCTGACCCGATACT
TGAACCTGGTCTCGTTCGGCAATAACTCGTTCCGGCTGCAGGACGCGCGCAAACGTNCTTCGGCATCAACGCGTCCG
ANCTGAATTGGCAGCAAGCGGCGCTGCTGGCCGGCATGGTGCAATCNACCAGCAGCTCAACCCGTA

(SEQ ID NO. 438)

:::Rv338T7.seq:::

CCCACGACTTCTCCTCGATCAGTTGGATTTGTACGAAGAGGCAACGAAAGCAGTGATCCTCGGGATGGTTCGACGCT
ACATCGACCCGCGGTTACGCCGCACAGCCTGCTAGATGCGCTGGGCGAGCAGGTCCACAGTTCCGCGCTAAGGCAC
GGCGTCTGTTCCCGTCCGGATCGCCATTCCGGCTCGGCGTCTGCTCCCATTCGATCAATAGGGCTGGCAGCTCCGTC
GGCAGGGGCTACGCCTACCCCGTCACG (SEQ ID NO. 439)

Clone Rv339

:::Rv339SP6.seq:::

CTCAAGCTTATGCGCGCCGGCCGAGGTCTGCTCAGGCAACCCCTGAAGTTTAGGGGACNACCTACTCAGCGCAAAAT
TTCGCTAATGTGAGTCCGCCCCACAGGGGNANATCAACCCATGTCGATCATGATCTACCCGATACGGATTGGCGG
TAGCGCCACGATCGTCNAAATNTCCGCTGAATCATCGGATAGCTGATCCGGCGTCAACGCGTTCGANTTCACCGC
GCAACAGCCGCCAGGCCGGCCGCANCGANCCGATCTCNTCGGGCCGCATGGGCCCAATCTTNTCG

(SEQ ID NO. 440)

::::::::::Rv339T7.seq::::::::::

GTGTGTGGTGGAAACCATCTGAGCAGTGTGCCAAACCGGGCAGACAGCTCCCAATTGACGTGAGCCCCTCACTTGC
TGGGTAAGCGTC

(SEQ ID NO. 441)

Clone Rv33

::::::::::Rv33SP6.seq::::::::::

CTTTACACTTCCTGCATCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATG
ACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGGGCGTGACGGCCACCGGGGCCACTCCG
CACCATCTGTACCCGACCAAGATCTAC

(SEQ ID NO. 442)

::::::::::Rv33T7.seq::::::::::

CAGGCATGCAAGCTTTAGCTGCCC GAATGCGTCACCCCGATGCGCCAGATCGGGGCTTCGCAGATAAAGCACGAACA
GGCGGGCAAACGTCNATCTCGGAGCCGGAAGGGCAATCAGCCGACCGTCGACGAACGACACCGGGCAGACCACTTAG
GCAGTGACGGCCGGCCGAACATTACGCGCTCGTTGATTAGGCGTTGCGTCTCGTCCGCGTTCATGCCGAGCAGCTTG
CGGCAGATCTGAACGCTGCTGTCCGGGCAGCGCGCCGGGCGTTGGGGTGCCTGCCCGAATGTGACGAAACGGAGC
CGGACCCGCTCTCGGCGGGCCGCGGACGGCGATCCGC

(SEQ ID NO. 443)

Clone Rv340

::::::::::Rv340SP6.seq::::::::::

CNCAAGCTTGCGGATGTTACCCCTGACAGCCTGAAGTATGTCNAAACACACGGCACCGGAACGGTGTGGGGGACCCC
ATCGANTTCGAGTCGCTGGCGGCCACTTATGGCCTGGGTAAAGGCCAGGGCNANAGCCCGTGCGCATTGGGGTCGGTC
AAAACCAACATCGGCCACCTGGAGGGCGGCCCGCGGTGTGGCTGGATNCATCAAGGCGGTGCTGGCGGTGCAACGTGGG
CACATTCCTCCCGCAACTTGCACTTCACCCGGTGAACCCGGCCATCNACGCGTCGGCNACGCGGTGTTCTGTCGCNACC
NAAAACCCCCCGTGGCCGGCGGC

(SEQ ID NO. 444)

::::::::::Rv340T7.seq::::::::::

GGAACCGGTAACCAGATCAGCTCGTCGACCTCACTGCCGGGGTGAATTCCCCACCGGTGCTGCGCGCTGCCAGTAG
TGCACCTTCTTGACGCTCGAAAAGGGGAGTCGGTCGGGTAGGTACCGTCAGGAGCCGCTACCCAGGTTGGCGCNA
TAGCCGGTCTCCTCGAGTATCTCCCGCACCGCCCCACCGGTGCGGTCTCACCCANATCCACTTTGCCCTTGGGCAGC
GACCAGTCGTCGTANCGGGGCGGTGAATGACAACGATCTCGACCGGCCCTTCN

(SEQ ID NO. 445)

Clone Rv341

::::::::::Rv341SP6.seq::::::::::

TACTCAAGCTTCAGAACAGGCCTGTTGTGGGCNACCCGGCTCGCCGAGTTCTGCACGCACCGCCTCAAGTGCGGCC
GCACCGCCGGCATCTCCCGGTACGCAGGGCCGCGGCCCGCGCCGAGCGACGGCGTGTTCGCGCAGTTCCGCGTCAA
TGATGCTGACCTGATCGGCCACCCGGGCGTTCTCGGCGTCGTCGCGTTCACTAATCGCGGTGCTCAGCAGCGTCTCGA
CAGCCACCACCGAGTGCGGACCACTGC

(SEQ ID NO. 446)

::::::::::Rv341T7.seq::::::::::

TAATGTCTTGCCAACGTCACCACAATCGCGATGAATTCAATCATGCCGCCAGGGCGGCCAACCAATGGTGGCCGCG
AGCGGCAGCTCGATCGCAGCGCGGAGGTTGCCGGCCGCCAGTTGATTACGAACAGGGTGAGGTCATAGGCGGGCAGG
ATAGTGACGAAGGCAAGACCTATATCTGCCGTGGAAGAAGAATCGAGTAGCCGGTCGACACAACGGAAGCGAAAGTG
TCCGCGATGTTGATGAGCGTCGCCGGTTGTGGCGGCGGTGGCGGC

(SEQ ID NO. 447)

Clone Rv343

::::::::::Rv343SP6.seq::::::::::

TACTCAAGCTTTCGTGATTCATCGCGCCAGCAGACCAACAAGAGCATCGGGACATACGGAGTCAACTACCGGCCAA
CGGTGATTTCTTGCCCGCCGCTGACGGCGCGAAGCAGCGCAGCGACCAATTACGANATGGCCAGCGCGTGCCGGGC
CAGCAGGTTGGTGCTCGGCGGCTACTCCAGGGTGCGGCCGTGATCGACATCGTCACCGCGCACCACTGCCCGGCT
CGGGTTCACGCAGCCGTTGCCGCCCGCAGCGGANNATCACATCGCCGCGATCGCCCTGTT

(SEQ ID NO. 448)

::::::::::Rv343T7.seq::::::::::

CCACCCGTGAATTTGGGATGGGCNAAAAGGCNAAGCACCGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGG
CTAGGGCTTCTCGCGGGAAGGCCCGAAGCTACGGCGTTTCAACAGCTCGCGTCGCCCTCGGACCGCGAATTCGGGG
ATGGCAGCAACCTGGTAGCACCTGGCCGGGCGATGATCTGCAGCGTCGCCGCGGGTAGTCGCCGCCCGGGCGGCTAC
AGTCTGAAACGCGATGACCATCGATGTGTGGATGCAGCATCCGACG

(SEQ ID NO. 449)

Clone Rv344

:::Rv344SP6.seq:::

TCAAGCTTTAGCTGCCGAATCCGTCANCCCGATGCNCCCAGATCGGGGCTTCGCANATAAAGCACNAACAGGGCGGGC
AAAACGTCNATCTCGGAGCCGGAAGGGCAATCANCCGACCGTCNACAAACGACACCGGCGANACCATTAGGCAGTGA
CGGCCGGCCGAACATTACNCGCTCGTTGATTAGGCGTTTCGGTCTCGTCCGCGGTTCATGCCGAGCAGCTTGCGGCANA
TCTGAACGCTGTCTGTCCGGGCAGCGGCGCCGGCGTTGGGGTGCCTGCGGAATGTGACNAAACGGAGCCGGACCCN
TCTCGGCG (SEQ ID NO. 450)

:::Rv344T7.seq:::

CCGGGGCCACTCCGCACAATCNGTACCNNACCAANATCTACACCATCGAATACGACGGCGTCGCGGANTTTCCGCGGT
ACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAATACTTTCATCCTGACGC
CGGAACAAATNGACGCNTCGGTTCCGCTGACCAATACGGTCGGTCCC (SEQ ID NO. 451)

Clone Rv346

:::Rv346SP6.seq:::

NCTGGCCTTTGGTCCACACTAANACAATACTCAAGCTTCCGGCCGAGAGCCGCCAACTCAGCATATCGTTAACCAGT
ATCCCGAGCCGATAGCTGGCGGGCTCGGGTGGTGGCCAGCGGCGTTCGACNAAAGGTGTGACCGTCATGAAACAGAC
ACCACGGCGGGCGTTCGGCGTGTGTCACCTGCTCGANATCTCAGCATCCGACGCGGTGTGATCGCGCTTTCCGGCGT
TNGTGGGTTCNCCGCCGAGCCCGGCAAGGCCGGCCGACACAACCCCGAAC (SEQ ID NO. 452)

:::Rv346T7.seq:::

CATCTGCCACCACACGACCGCGGTGCGGACGCGGCTGACGCGCTGGTGGTCAGCATCGTGGCGGCTGTGCTGTTG
TATGCCAGCTTCCCGCCGCGCAACTGCTGGTGGGCGGCGGTGGTTGCGCTCGCATGCTGGCCTGGGTGCTGACCCAC
CGCGCGACGACACCGGTGGGTGGGCTGGGCTACGGCCTGCTATTCCGGCTGGTGTCTACGTCTCGTTGTTGCCGTGG
ATCGGCGAGCTGGTGGGCCCCGGGCCCTGGTTGGCACT (SEQ ID NO. 453)

Clone Rv347

:::Rv347SP6.seq:::

GACAATACTCAAGCTTGACTGGCCACCCACCGCATGACCACCGACAGGCCCGACTGGTTCGTACCACTCGAACGCCGG
GGTGTGATGTCCAGCCGCTGAANTCGTCTGCGCGCGCAGGCCGTCNAACAGGTACAGGGCGGGCGAATTGGCACC
ACCACTTTGGAATTGGACCTTGATGTACGGGCCATCGACGGCGACGGCACCTGCAGGTACTCCACCGCAAGCCCCG
CCGGGAAAATGCCCGCGGTTCNCCGTGCCACCGACGGCGCCGANCAAACCCGACACTAGGGCCGCGCCNACGGCCCC
GACCACNANTCNACGCGACATACCCGTGACGGCGCCACNAACCCTGTCAACA (SEQ ID NO. 454)

:::Rv347T7.seq:::

CCTCCAATCGGCGGGGAAGCGACNCCAGCCTACCGAGCTTGGAGTCCANGACGCCAGCGGGCGGCTCGGTCTGCGTC
GTGGTGCCGCGGGGTGGCGTTGGCTGGCAACGATCTCCACCCAGCCGGTTCGGGTACCCACGATCTCGGCATANACG
CGGGCCGAGGCCGGTTCGATACCGTATTGCGTCAATTGGGACGCGGTTGTGATTGCGGTAGCTCGGTTGCCACACCC
GTCAGGGGTTGACGTTGGCGGGTTCGGCGGGCCCCANACCGCTGTACCATGCCCGCAAGCCGACCTGCGGCGCC
ACCAACTGCAGCACCANCATGTCGCCGTGCGCGCCGCGATCACATGG (SEQ ID NO. 455)

Clone Rv348

:::Rv348SP6.seq:::

CTCAAGCTTTTGGAGCTGCGCGGGGCANCTTCGCCGGAATTCTACTANCGAGAANTCTGGCCGATACGGATCTG
ACCGAANTCGCTGCGGTGCANCCACCCTCATTGGCGATGGCGCCGACNATGGCGCCTGGACCGATCTTGTGCCGCTT
GCCGACGGCGACGCGGTAGGTGGTCAAGTCCGGTCTACGCTTGGGCCTTTCGGGACGGTCCCGACGCTGGTTCGGGTT
GCGCCGCNAAAGCGGCGGGTTCGGGTGCCATCAGGAATGCCTCNCCGCCGCGGCACTGCACGGCCAGTGCCGCGGCA
(SEQ ID NO. 456)

:::Rv348T7.seq:::

CNCCAGCTTGATTGGTCTGGTTCATTGGCCAGCTGCGCGAGCCTGGCTCACTTCAACTACGACGACCGCAAACAATT
GCCGCTTCGGATCCGAGTTTCGGTTGGGTACGCGGCAATGGAGCACCATTCTCGGTGAATCAGACTATTCTGAGTA
CTTGATCATCACTCTGCACACGACCTGCGAACCCCGCGCGGCTTTCGGACCTGGAGCAGCTGGCGCAACGTGTGAG
CCAGATCCAGGCGTTGCCATGGTTCGCGGTGTGACCCGGCCAAACGGGGAAAC (SEQ ID NO. 457)

Clone Rv349

:::Rv349SP6.seq:::

CAATACTCAAGCTTGACTGGGCGCGCACCTTCGGCGCCACCCACACCGTCAACGCCCGCGAAGTCNACGTCGTCCAGG
CCATCGGCGGCTCACGGATGGATTGCGCGCGGACGTGGTGTGATCGACGCGGTTCGGCCGACCGGAAACCTACCAGCAGG

Clone Rv160

.....Rv160SP6.seq:.....
ATACTCAAGCTTCGCACGCTCGGCGCGCGCGGTACCGCCAGGTGCGCCAAACAGATCGTCGATGTTGCGCTCGTCCGC
CTCGCGCACGTGGTCTGTCAACAGTCAACGTTAACGCCGCCGCACATGTCTGCGGCCGGGCAAAAACGTGAAAAACG
AGCGGGCGACTGCNATGTCATGACACCGACGGCCGCGGATGGGCCAGGGTCTGGCAAATTCGATCTGTGCGGCCAGT
GCCAGCAGCGTCGCCTCGTCATACGGCCGCGCGACGAGTTGAACCGACATGGGCAGGCCGTGCGCGTCAAGTCCAC
GGCACCACGGGCGCGGGCTGGCCGGTCAGATTCCAAATTGAAAGTACGGAACCGCTGCACCACAA (SEQ ID NO. 121)

.....Rv160T7.seq:.....
ATCGTTTCGACCAGGCGCTCCATCCGGCGAGTGGATACTCCCAGCAGGTAGCAGGTGCGCCACCACGCTGGTCAGTGCG
CGTTCAGCTCGCTTGGCGCGCTGCAGCAGCCAGTCCGGGAAATAGCTGCCCTGGCGCAGCTTGGGGATCGCGACGTGCG
ATGGTTGCGGCACGGGTGTGAAATCACGGTGGCGGTAGCCGTTGCGCTGATTGGACCGCTCATCGCTGCGTTGCGCGG
TAGCCCGCCCCGCACAGGGCGTCGGCTTCAGCCCCCATCAAGGCGGCGATGAACGTGAGAGCAGCCCGCGCAGCAGA
TCCGGGCTCGCTGTGCGAGTTGGTCAGCCAGAAGCTGCTCGGTGTCGATAAGATGANAAGAAGTCATTGCGTTATTT
CCT (SEQ ID NO. 122)

Clone Rv161

.....Rv161SP6.seq:.....
ATACTCAAGCTTGGGTGTTGCCGATCACCGAAGCCGCATGATCAGCCACGTTTCGCGCCGCCCGGCATACGGCGGGCG
TACCGATCTCCGCGTCATACACCCGCGGGTAATCGCCGACGGTGCCGGTTGCGGAGCCGAAGGTGACGACGCTGATTG
AATCGAGTTCAGGTCCAGCGGGTGGCGCAGCAACGGCGCGAGCTCAACNACGTCAATCACGTTGTGCTTTCTACGG
TCACCGACCCGGTGACCGTAGTCGCGCGGTGCGCTCGGCCGAGAAGTTCACCGCCACCACCGCGACAACGTCTTGCA
CGCGGACGCCACCCCCCGAT (SEQ ID NO. 123)

.....Rv161T7.seq:.....
GCGCNAACAGCTCGCGGCAGCCACGACGTGCTGCGTCGGATTGCCGGCGGCGAGATCAATTCCAGGCAGCTCCCGGA
CAATGCGGCTCTGCTGGCCCGCAACGAAGGACTCGAGGTCAACCCCGGTGCCCGGGTCTGGTGCACCTGCCGATCGC
ACAGGTTGGCCCAACAACCGGCCGCTTGATGCCCGGTGCGCAAGCCCGGAGTTGCCAAACCCAGCGTGATCAGGCTCG
GCTCGCGAGTTCGGCGAAAAAGTGGCTCGCTGATCACCTACCATCGGCCAGGATCTGCGTGTGTCATCACGACGCTCGC
CAAGGAGGTTGTTGTTGCTATCGACGGCCTTTAGCCAGATGTTCCGAATCGACTATCCGATAGTGTCCGCGCCAAT
GGACTTGATCGCCGGCGGTGAGCTGGCTGCCGNGT (SEQ ID NO. 124)

Clone Rv162

.....Rv162SP6.seq:.....
ATACTCAAGCTTTCTCCGATACCCGCCATGTGCGGCACATCCAGGACTTCTGGGGGATCCGCTGACAGCGGCGGGAT
CCCAAAGTCCGGATGATCGGGCCGCTACGTCGTGGTGTACCTCGTCGGTAACAACGAAACCGAAGCGTATGACTCGG
TCCACGCGGTGCGGCACATGGTGGACACCACCCGCCACCGCAGGGGTGAAGGCCTATGTACCCGTCGCGCAGCAC
TCAATGCCGACAGGCCGAGGCCGAAACAAAGTATCGTAAGGTACCGCGATCACGAACATGGTGATCGCAGCAA
TGTTGCTAGTGATCTATCGCTCCG (SEQ ID NO. 125)

.....Rv162T7.seq:.....
CCATGAGCACCGCCAGCCGAGCAGAGGCCAACTCCGCCGACGAGGCCGTTGGACTTGTGCTGCTGGACAAGGGG
TTTAGCCGCCGAAGCAGTGACGTACATCGGCGAAGAGCAGTTGCGCTGTCGACCGACGGCGCAAACCGTGAGGCTAGG
GAAGCGAGGAGCACATGGCCGCCGACCCGCAATGTACACGCTGCAAGCAAACCATCGAACCCGGATGGCTATACATCA
CCGCCCATCGCCGCGGTCAAGCCGGGATCGTCGATGACGGCGCAGTACTGATTACGTGCCCGGTGAATGCCGCACCC
CGGGGAGCACTTTCCGCCAAAATAACCCGGTTGG (SEQ ID NO. 126)

Clone Rv163

.....Rv163SP6.seq:.....
CGGGTGTCAATTGGCCACCGGCGGCGGTGTCCGGGAAATGGCGGGTCCCCGGTGGTTTTGCTGAGGAGTGCTGAACCG
TAGTCGAAGTGGGCGGCGTCAGACTCCACCCAGCCAGGAGCGCGGAANCTGAATCCTCCAACCGGGTTGTCNATC
CGGACAGGTTGGGGTGCCTTTGGGGCAATNACAGGTGGCGGCGGTGCGTTGCGGTCGGCCGGCGGAGGTGCTGCNTTG
GGATCCCCGGTGGGCATTGCGCNTGTTGGCGGCGGCGGTGGTGGGGGGGCAACACGTGTCNCCGGTGGCGGTGGC
CCT (SEQ ID NO. 127)

.....Rv163T7.seq:.....
CCAAGATCTACACCATCGAATACGACGGCGTCGCCGACTTTCCGCGGTACCCGCTCAACTTTGTGTCGACCCTCAACG
CCATTGCCGGCACCTACTACGTGCACTCCAATACTTCATCCTGACGCCGGAACAANTTGACGCAGCGGTTCCGCTGA

CCAATACGGTCCGTCCCACGATGACCCAGTACTACATCATTCGCACGGAGAACCTGCCGCTGCTAGAGCCACTGCGAT
CGGTGCCGATCGTGGGGANACCCACTGGCGAACCTGGGTTCAACCAAACCTGAAGGTGATTGTTAACCTGGGCTACGG
CGACCCGGCCTATGGTTATTCGACCTCGCCGCCAAATGTTG (SEQ ID NO. 128)

Clone Rv164

:Rv164SP6.seq::

AGCTTCCCAGATTCCGGCTTGGATCAAGACCCAGTCCGCGGGCGCGATCCGGCNGCTCGGTGACTACATCAAGCCAC
AAATCGACGGCTTTCGGGGTGCCGATACCGATGACGTGGCGGATGTCGAGTGTTGAGTTCTCGGCGGGGCGGATGCTC
ACCTGGCCGATCACCTGCCTCTCGTTGACGATCGATCGTCTATGCCGCCGTCTCTGCGGGAACAGGCCNCCAGTACATC
GCCACAGACGGGATCCACCCGCATTTCCGGCTACGGTTGCTCGTTTCGGTGTTCCGACTAGTCGGTCTGGTGACGTGC
CGGTGATGCGGACCGGTCCTAGCACTGACCAATGGCCAAATGCGGGC (SEQ ID NO. 129)

:Rv164T7.seq::

CGGGGGGCTCTTAATAGTGTAGGAAAGAGCTCTACATATTCAGGAGGATTACCATGGCTCGTGCGGTCCGGATCG
ACCTCGGGACCACTCCGTCGTCTCGGTTCTGGAAGGTGGCGACCCGGTCGTCTCGCCAACTCCGAGGGCTCCA
GGACCAACCGTCAATTGTCGCGTTCCGCCGACCGGTGAGGTGCTGGTCTGCCAGCCCGCCAAGAACCAGGCAGTGA
CCAACGTCGATCGCACCGTGCCTCGGTCAAGCAGCATATGGCGAGCGACTGGTCCATAGAGATTGACGGCAAGAAAT
ACACCGCGCCGGAGATCAGCGCCCGCATTTCTGATGAAGCTGAAGCGCGACGCCGAGGCTACCTCGGTGAGGACATTA
CCGACGCGGTTATCAGACGCGCCGCTACTTCAATGACGCGCCAGCGTCAGGCCACCAAGGACCCGGCCAGATCGCCGG
TCTCACGTGCTGCGG (SEQ ID NO. 130)

Clone Rv165

:Rv165SP6.seq::

ATACTCAAGCTTCATAACAGGCCTGTTGTGGGCGCACCCGGCTCGCCGAGTTCTGCACGCACCGCCTCAAGTGCGGCC
CGCACCGCCGGCATCTCCCGGTACGCGAGGGCCGCGGCCCGCGCCGCGAGCGACGGCGTTCGCGCGAGTTCCGCCGTC
ATGATGCTGACCTGATCGGCCACCCGGGCGTTCTCGGCGTCTTCGCGTTCACTAATCGCGGTGCTCAGCAGCGTCTCG
ACAGCCACCAACCGAGTGGCGACCACTGCTCCACACGGACCGCAGCGATGCCGTACCTCACCGTCCAGCGGTCC
ACCACGACACGGTCTGTCACCAAGCGCGGGGCTTCAACCAACCCAGGCGGTACCGCCAGGCGGATCGCCACACCCGCC
ACCATCCCGATGCAGCCAGGCCGGGAGTAAGA (SEQ ID NO. 131)

:Rv165T7.seq::

CTGGTGCTGGACGGAGCCTAGTACAACCTCCTCTCCAATGCTCTTGCCCCGATCGCGGGCGACAGGATGACCCAGGAC
ATCCTGCCGCCCCGAAGTACTGGAAAAGCTCACACCCGAGTTCTGTCGACCCGGTGGTGCCCTACCTGTGCACCGAGGAG
TGTGCCGACAACCCATCGGTGTACGTCTGAGTGGTGGTTAGGTGCAGCGAGTTGCGCTGTTTGGCAACGACGGCGCC
AACTTCGACAAACCGCCGTCNGTACAAGATGTTGCGGCGCGGTGGGCGGAGATCNCCGATCTGTCCGGTGCGAAAATT
GCTGGATTCAAGTTGTAGAACTAAAT (SEQ ID NO. 132)

Clone Rv166

:Rv166SP6.seq::

ATACTCAAGCTTTTCCGGCGTCGTCCACCTGACCCAAAAAGCGCAGGTGCGCCGCCAAACGGCCCGCTGGCCGCGCA
ACTGGTCCGCGTCGCCGTGGCCGACAATCAGTAGCTGGACATCCGGAAACCGCTGCACCACCTTCGGCAGCGCGTCAA
GCAAAACGGCCATTCC (SEQ ID NO. 133)

:Rv166T7.seq::

TTTCAGATCTCATTTTTATGACATGACTGGAGATCTGTCTAGATTGCAGCTCCTGTGAGCGTGGGTACCGGATTCAAG
CCGGTCCGTCACGCCGCGGTGGTACCGGCTTTGCGGCAGTGCTCGGCCCTCGAGTTCCGGCGATCGCGCGCGAAGTGCGT
TTTCGCGACCAAGATCGCGGCCTAATGGCCGGCGATGACCGCGATGACCAGCGCGATCCAGGAAAAACCGTTCCAACC
AGTGCTGGGCGGCCATCCCCG (SEQ ID NO. 134)

Clone Rv167

:Rv167SP6.seq::

ATACTCAAGCTTCCCGACCACAAGTTGAACAGCACCGATTTCGGCGAGCACTTCGTCAACTTCCAGGGTGCCCGCACC
AAGTATTTGACAAGTATTTCCGTGGGGCCGCCGCCCGCGCGCGCAGGTGGTCATCCTGGCGCGGGGCTGGAC
TCCCGCGCGTACCGGCTGCCTTGGCCCCAGGGACACGGTTTTTGAGCTGGACCGCCCGCAGGTCCTTGATTTCAG
CGCGAGGTGCTCGCCAGCCACGGTGCCCAACCGCGCGCCCTGCGCCCGCA (SEQ ID NO. 135)

:Rv167T7.seq::

GTGTGCTGTCAATTCAGAGCTGAGCCTGATGCACTCAACTTACTGAGCATGCTAACGCTGGTGGTGGGGTCTGTTC
CCGCGTGTCCGACGGGCACACGCTCGGGCGTAGCTGGGAGAGGCCCGGTCAAGCCCGAGAGCAGTGCTCAGTCCG

CCAGCTTGACCGACTTTTCGATGAGAACGCGCTTCTCGCCGTATTGAACTGGCGTGCTGACGGTCGCTGAGCAGCGCTC
GCCGAGTGCGGCCGCTGATTCTTTTCATCGAGCCAGGAGGCGCATTCGTGTTTCGGCCGCCTGCGGGTCGGCCCCATCGT
CGACGCGATCCGTCACCCACTCCTCGATCAGGTCTGCCTCATCGAACGGGCCAACGGTGCTGTCGGAGTATGTGTGCG
TGGGCACGGCGAGCCGGGTGCTGTGGTACACCCACCGTTGCATGACCAAGTTGACGCCCTGACTGGCTGAGCACCAGCGA
TCCGCTCACAGGTCGGAACGTTGGTG (SEQ ID NO. 136)

Clone Rv169

.....Rv169SP6.seq:.....
ATACTCAAGCTTTTGGTCTAGCCGGCCGAGCCCGATACAGGTGTATTGGCCACCGGCGGGGCTGTCCGGGAAATGG
CGGGTCCCCGGTGGTTTGTGAGGAGTGCTGAACCGTATGCGAAGTGGGCGGCGTCAGACTCCACCCAGCCAGCAGG
CAGCGCGAAACTGAATCCTCAACCGGGTGTGATCCGGACAGGTTGGGGTGCCTTTGGGGCAATGACAGGTGGCGG
CGGTGCGTCCGGGTGCGCCGGCGGAAGTGCTGCGTTGGGATCGCCCGGCTGGGCATTCTGCGTGTGGCGCGGCGCGG
TGGTGGGGGGGCAACAGGTGTCTCCGGTGCGGGTGGCGCTGCACC (SEQ ID NO. 137)

.....Rv169T7.seq:.....
GGGGCCACTCCGCACAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCGCCGACTTTCCGCGGTAC
CCGCTCAACTTTGTGTCGACCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAATACTTCACTGACGCCG
GAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACTACATCATTCGCACGGAG
AACCTGCCGTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGTTCAACCAAATTG
AAGGTGATTGTTAACCTGGGCTACGGCGACCCGGCCTATGGTTATTGACCTCGCCGCCCAATGTTGCGACTCCGTTT
GGGTGTTTCCAGAGGTGACCCCGGTGCTCATCGCCGACGCTCTCGTCGCCGGGACCCAGCACGGAAAT (SEQ ID NO. 138)

Clone Rv16

.....Rv16SP6.seq:.....
TTCTNTCTTCCNNATTCTGNNNTCTCNTACTACCNGGGCCNCAAAACACCTTGGCNAACGCTCAAAGGCGNTACNGG
CACCAAGGCCCCACACGTACCCCTGTGACCTCCTGCGCCGACCCCGCCGAGGTCTGGCCGTTACCACTGAACGGGC
GAGCCGGGAGTCTGGTACGCATCGAACAAGAGCAAGGTGCATGGGCGGAGTTGTTCCGCCNCTTTTTTATGACGGG
GTGATCCATTGAGGTCCGTGCGCGCGTGGTGCAGTGGCGGTCACTCCAGGTACTCGACCTCNAGACGAGAGG
ACTCGATCCCATCTANGTGTGGACNAAACAGATCTTCTGTCCGACGACTACACACCACCCAGGCCATCGCCGCCGCC
GCGATGCCAACTTNCACNCCGTNCTGGCCCCGGCGGCGGCGCTCCCCGTTGTCAAACACCTGCCGTGTTCTGTTACN
CACTGCCCAACATCNAGCCGANCNATCCNAGGTCCGTCCAACGCCCTCCGCGGCTCNCCAACCTNCTCCNCTGATCN
TCCGCACCAAAACATGCCGACTCCNTGCNCCNATTGCTTGNATCCCT (SEQ ID NO. 139)

.....Rv16T7.seq:.....
CCGCTATCGGTGCGTGTGCTTGGCGGCGTTCGGTATCAACACCGCCACGAAATGGGGCACAAGAAGGATTGCTGGAG
CGGTGGCTGTCCAAGATCACCTCGCCAGACCTGCTACGGGCACTTCTACATCGAGCACAACCGTGGCCATCACGTC
CGGGTGTCCACACCGGAGACCCGGCGTGGCGCGGTTCCGCGAGACGTTGTGGGAGTTCTGCCCCGAGTGTATC
GGCGGCTTGCCTCGGCCGTTTATTGGAGGCCCAACGGTGCCTCGGCTCGGCGTCAGCCCCCTGGAATCCCATGACG
TATCTGCGCAACGACGTGCTCAACGCGTGGCTGATGTGCGTGGTGTGTTGGGGTGGGCTGATCGCGGTCTTCGGCCCC
GCGCTGATCCCGTTCGTATCATCCAGGCAGTCTTCGGCTTCAG (SEQ ID NO. 140)

Clone Rv170

.....Rv170SP6.seq:.....
ATACTCATGCTTGCCGAAGTTCGGATGGGTGCGCGCGGCGANCCAGCGAAGTCGCTAGCGTGGCCGTGTTCTTGGCT
TCGGATCTATCCTCGTACATGACCGGCACCGTGTGGACGTGACTGGCGGCCGTTTCATATGACACCGAGATCATTCG
CACGGTACGGCAATTCTGTCAAGAAGGAAATCTTTCCCAATGCACCGGCCCTCGAACGTGGCAACAGTACCCGCAAGA
AATCGTCGATCGGCTGGGTGTTATTGGCTTGTGCGTTCGCCGGCTGCAAGGGTATCGACACCACCGAGTTCATTCTCC
GGCGGTGCC (SEQ ID NO. 141)

.....Rv170T7.seq:.....
GGCGTCAACGGTGTGCGCACCGGCGTCTGCAAGTGGTAGGCTGCAAGTTGTGCATCAGGCCGATGCCGCGGCCCTC
GTGGCCACGCATGTACAGCACCACGCCGCGCCCTCACGGGCGACCATCGCCAGCGCGGCGTCCAGCTGAGGCCCGCA
ATCGCAGCGGCGTGACCCAAACACATCGCCGGTCAAGCACTCCGAATGCACCGGACAGCAGCTGTCACCGTCCGC
GTTGGGCCGCGGATCTCGCCGCGGACAGCGCGACATGTTCCACGTCTCTAGATGCTGGTGTAGCCGATGGCGCG
AATCTCCATGACGAGTCGGAATCCGCGCCTCGCG (SEQ ID NO. 142)

Clone Rv171

.....Rv171SP6.seq.....
ATACTCAAGCTTCGGCCTCGCTGCAGGAGTGGGAGCCGCGAGGGCTGGAAATCCGAAAAACGAGCCGGTGATCGCACTG
TCGCCGATCGGGGCCGACCTGGTTGGTGTACCGATGAATCCGCACCCAAAATGTGGCTGCGGTGGCGTTTCTTGAC
TCCTTGGCGTCGACTCTTGTGGCAGCCACCGAGCGGTTGGTCCAGGATCTGGATGGGCAAAGTTGTGCGGCCCGGCCG
GTGACGGCCGATGAGCTGACCGAGGTCGACAGCGCCGTGTTGGCTGACTTGAACCGACATGGATTGCCCCGGTTGG
CGTCACCTCAAGCATTTCAATGGTTAT (SEQ ID NO. 143)

.....Rv171T7.seq.....
ATGCGTCACCCGATGCGCCAGATCGGGGCTTCGCAATAAAGCACGAACAGGCGGGCAAACGTCTATCTCGGAGC
CGGAAGGGCAATCAGCCGACCGTCGACGAACGACACCGGCGATAACCACTTAGGCGTTGAACGGCCGGCCCAAACATT
ACGCTCCGTTGATAAGGCTTTCGGTCTCTTCCCGGTCATCCCAAGCACCTTGCGGCAAATTTGAACGCTTTCCTGT
CCGGGCACCGCCCCGGGCTTGGGGTCCNTCCGA (SEQ ID NO. 144)

Clone Rv172

.....Rv172SP6.seq.....
ATACTCAAGCTTCAATCGCGCCGCCACAATCCAAATATGCGTCTAGCGTCTCGATGAGCGTCGGTCCGGCATCGGCTA
GGGGCCGCATCACGTGCGTATGAGGGCCACGATCGCCCAAGGCGTCGCCCATCAAGGGCGCGTTCGGGCAAATTC
CCCTATCCAGCACGGGCCGCGCGCTCCGCNCCAGCGGCGACGGCGTTCATCCCGGAGATCGCCTCGCTAGCGCTGC
GGTGCGCCGCGGTGAGCATGGGCGCCGTGGGGCCGATGACCACCGGGGCGT (SEQ ID NO. 145)

.....Rv172T7.seq.....
TTCGGCGGGTCTGTAGATTGCGGTGCGCCACCCACAGGCACTCATGAACCGCAGCCACGATCGATCTCGGTGG
(SEQ ID NO. 146)

Clone Rv173

.....Rv173SP6.seq.....
GCGCACCATCGCCAGTAGGTGCCCCTGGTGGGCGCGTCGAGCCACCCGAGCGGAACGCGAGTCCGAACAGCAACAG
CAGGACGGGCGCAACCAGGGCGGTGACCATGCCCCCGGCGGTGAACATCAACCACAGGAAGGGCTCCGCCGAGCGTCC
GCGCGACC (SEQ ID NO. 147)

.....Rv173T7.seq.....
CATCGTCGAACCTCGGTCCGGTTGNTAGNACCGCAGCACCAAACGCACCCACCGACCCCCACGCTTCACGCCAACCC
TTTAGTTTCATTGGCGTGAACAGCAGCGTAGCCGGTTGCCCGATATATGTGGAAAAATCGTTCGGACGTACAAAAAA
GTTCTGACGCTGGCGTCAACTCGAAATGCCTCGGAAGTCAATGATGATCCATCAGTCAATATTAAAGTCG
(SEQ ID NO. 148)

Clone Rv174

.....Rv174SP6.seq.....
ATACTCAAGCTTGTCTGCTGCCTCAGCGTATGCATCCAACAGCGCATCGCGATCAACGATCAGGCGCGCCGATTTGGG
GCCGCGGGCAGTGGCACTGGCCAGATGGCCGTTTTTTTCGAGAACTTCAACGCTGAGCGCTGCTTCCCATCGAGAG
ACCGGTGGCCTCTACAACCGATGCGACAGTTGGACGGCGATGTTCCGACGACGCGTTACATACGGCAAGTNTGGC
GCGG (SEQ ID NO. 149)

.....Rv174T7.seq.....
TTGTCCAGGCGGGGAATCGGGCAGGGAGACGACACCTTCGTTGCGTTTCGATCGTCGGAACGGGTAGTTGGCCGCGAC
CACGTTGTTTCGGGTGAGCGGTTGAAAAGTGTGACTTGCCGACGTTGGGCAGGCCACGATCCCCAGGCTCAAGCT
CACAGA (SEQ ID NO. 150)

Clone Rv175

.....Rv175SP6.seq.....
ATACTCATGCTTGGCGCCTGGGTGGCAGCCACCTGCCACCACACGGACCGCGGTGCGGACGCGGCTGACGCGCCTG
GTGGTCAGCATCGTGGCCGGTCTGCTGTTGTATGCCAACTTCCCGCCGCGCAACTGCTGGTGGGCGGGCGGTGGTTGCC
CTCGCATGCTGGCCTGGGTGCTGACCCNCCGCNCAACACCGGTGGGTGGGCTGGGCTACGGCCTGCTATTCCGC
CTGGTGTCTACGTCTCGTTGTTGCCGTGGATCGGCGAGCTGGTGGGCCCCGGGCCCTGGTTGGCACTGGCGACGACG
TNCGCGCTGTTCCCCGGCATCTTCGGTCTGTTCCCGTCTGTTGCGCGGTGACCTGTTGCCGGGTGGCCCC (SEQ ID NO. 151)

.....Rv175T7.seq.....
CGCCAATTACGATATCGTTAACGATATCCCGAGCCGATAGCTGGCGGGCTCGGGTGGTGGCCAGCGGGCGCTGCGAC
GAAAGGTGTGACCGTCATGAAACAGACACCACCGGCGGCGTGGCCGTCGTCACCTGCTCAGATCTCAGCATCCGC

AGCCGGTGTGATCGCGCTTTCGGCGTGTAGTGGGTCGCCGCCGACCCCGGCAAAGGCCGGCCCGACACAACCCCGGA
ACAGGAAGTCCCGGTACCGCGCCCGAAGNACTTGATGCGCGAACNCGGAGTGCTCCAAACGCATCCTGCTGAT

(SEQ ID NO. 152)

Clone Rv176

.....Rv176SP6.seq:.....

ATACTCAAGCTTGGGCACTGACTTCGGTACCCCTCCGCCTTTGGCCAGCAGCAGCCACAGCGCGGTTCCGGGACCGA
ACGTGGACATCAATAGCCCGGAATCGGTGTGTGCAAGTTGGTAAACGGTGTGATCCCAAGCTTTGCCAGCCTTTTCG
TAGTCTTGGGCCCCACACCCACAGTGCTTCGACGGTACGGTCACCCATGATGGCCATCCAGTTGGCATCGGTGAGCT
GATAAATGCCAGCTGGTTTCGCCAACC CGGTAGCGATCTTGGCGCGCTGCTTGTGTCACTGATACCTATCGAGCAAG
ACAGCCCGGTTTGGCAGAAAATGACTTTTCGGATCTCTTCGGCGACTTCGATGGGGTCGTCCGGA (SEQ ID NO. 153)

.....Rv176T7.seq:.....

AAAGTCCTGTGCCGGTTCGCTAAACACCCGGCGGACACTCAGACGGTGCTGGTGGTGCGGCATGGCACC CGGGCAGC
AAAGCGCACTTCTCCGGGGACGACAGCAAGCGACCGCTAGACAAGAGGGGTGCTGCGCAGGCAGAAACGTTGGTACA
CAGCTGCTGGCGTTCCGGCGCCACCGATGTTTATGCCGCCGACCGGGTGCGCTGCCACCAGACGATGGAGCCACTCGCC
GCGGAACTGAACGTGACCATAACA (SEQ ID NO. 154)

Clone Rv177

.....Rv177SP6.seq:.....

ATACTCAAGCTTGGGTTCACGCCCCGCGCAGCCACGCCGTACCTTTCCACGAGACCTCACCTGCCGATCCGAAATGG
AATCGGCCGTGACGGAATTGGCGCACCGAACACCCAACGAGGTGGTGGCTTCGTGCGCAACCGTCACCCGAGTCGCGG
CCACCGTGCGCACGGCGACGTTCTACACCCGCACCAAGATCCGAAAGCTGCAAGCTCCAGCACCGATCCCGACGTCA
TCACCGCTGCCGCCCGGCACGTCTTGACCTATTCGAGCTGGATCGGCCCGTCCGGTTGCTGGGAGTGCGGTTAGAAC
TGGCCTAGAACCGCGGGGCACACCGCNCCTGGGCGGGGCGAATTCTTGACCGCNC CGGCC (SEQ ID NO. 155)

.....Rv177T7.seq:.....

CGCGGTTGGCGTAGTTGGACGGGTCGCCCTCCGAGGCCAATGATGACGATGACCACGCCGATCACGATGGCCACCGAG
AGGGACAACAACAGAAAGCTGACGAATCCCTCCTTGGCGGGCGGGGCTTTGTGGTCCCGGTCCGCGATGGGCGCGAAT
TTACGGCCCCGTCCCCAGGCCGCCGCGAAGCAGGGTCCCCAGCCAGTTGGCGTAGGCGGAATTAACGATCAGCGCCA
CCGCGATAACCTGCCATGCCTCGGGCATATCGATGTGCGGCCAGAACAGGCCGAAC (SEQ ID NO. 156)

Clone Rv178

.....Rv178SP6.seq:.....

CCAACAAGAGCATCGGGACATACGGAGTCAACTACCCGGCCAACGGTGATTTCTTGCCCGCCGCTGACGGCGCGAACG
ACGCCAGCGACCACATTCAGCAGATGGCCAGCGCGTGCCGGGCCACGAGGTTGGTGCTCGGCGGCTACTCCAGGGTG
CGGCGGTGATCGACATCGTCACCGCCGCACCACTGCCCGGCTCGGGTTACGCAGCCGTTGCCGCCCGCAGCGGACG
ATCACATCGCCGCGATCGCCCTGTTCCGGAATCCCTCGGGCCGCGCTGGCGGGCTGATGAGCGCCCTGACCCCTCAAT
TCGGGTCCAAGACCATCANCTCTGCAACAACGGCGACCCGATTGTTTCNGACGGCAACCGGTGGCGAGCGCACCTAG
GCTACGTGCCGGGATGACCAACCAGGCGGCGGCTTTCGTGCGGAGCAGGATCTAACCGCGAGCCGCCCATAGATTCC
CG (SEQ ID NO. 157)

.....Rv178T7.seq:.....

TAANACCCGTGTAATTTGGGATGGGCAAAAAGGCCAAGCACCGCGTGCCACGAACGCCGGGAGGGACAATCTCGGGC
GGCTAGGGCTTCTCGCGGGAAGGCCCGAACGTACGGCGTTTCAACACGTGCGGTCNCCCTCCGACCGCGAACATTCCG
GGATGGCAGCAACCTGGTAGCNCCTGGCCGGGCGATGATCTGCAGCGTCGCCCGGGTAGTCGCCGCCCGGGCGGCT
ACAGTCTGAAACCGCATGACCATCGATGTGTGGATGCAGCATCCGACGCAACGGTTCTACACGGCGATATGTTCCGC
TCGCTGCGCGGTGGACCGGTGGGTCTATCCCGGAGACCGACNTCCCGATCGAAGCGACCGTCTCTCGATGGACGCC
GGCGGCGTCACCTGGGTTTGCTACCGCCTGGCGTGCCCA (SEQ ID NO. 158)

Clone Rv179

.....Rv179SP6.seq:.....

GTCCGCAAAAGACTCAGCGGCCGACTTTGCTCGCAGCTGGCGGTACCGCGCCACCGATTTCGATGCCGTGGTCCGGGAA
GAATGCCTCCCGAAATCGCACGGCCGACTCCAGTTCCGGCGAGCATCCGCGATGCCAGCTGCGGCTGCGCCCTGCCGGC
CACGGCACCCACATGCGGCAGTTCTGCCACCTGGGCCAGCGCCCCGCCCGCAAGTCCAAACAATAGAACTGCACCCG
GCCCGCATCGTGGGTAGCAGCCAACGCCATGATCAGCGTCCGCGAGCGCGGTTGACTTGCCCGTTTGGGGTGACCTAC
GACCGCGACATTGCCTGCGGCCCCGACAAGTCGATCGTCAGCGGCACCCN (SEQ ID NO. 159)

.....Rv179T7.seq:.....
CGTGGCCACGAACGCCGGGAGGGACANTCTCGGGCGGCTAGGGCTTCTCGCGGGAAGGCCCGAACGTACGGCGTTTCA
ACACGTGCGCTCGCCCTCCGACCGCGAACATTCCGGGGATGGCAGCAACCTGGCAGCTACCTGGCCGGGCGATGATCTG
CAGCGTCGCCCGGGTAGTCGCCGCCGGGCGGTACAGTCTGAAACGCGATGACCATCGATGTGTGGATGCATCATC
CGACGCAACGGTTCTTACACGGCGATATGTTNCCTCGCTGCGCCGGTGGACCGGTGGGTCTATCCC (SEQ ID NO. 160)

Clone Rv17

.....Rv17SP6.seq:.....
ATACTCAAGCTTTGCGCGGGCGCCGAAATGTGAACGCACCAAAACCCGCCCGCTGCGGGTTCGGCGGGCCACTCGACCT
CGAATTTTCGCCGCCGTGACCATCCAGCCCGACGGCAGTTGGGCACCCGCCCGCGGTGCGCGGCATAACTGTTGGCGT
CGCCGTCTATAAAGCTCGAACAGCACCAGAACCGACTCCACCACCGGCCGGTGCGCCTCAAAATCCACGCCGATCTCCA
CATACCGGGAAAACGTCGGTGTCCCATCGGGTTTCGGCTTGGCCGCCAGCTGCACACCACCGGTGGCCTCGGCCACCT
TCGCGGCCTGAGCGCAGCTACNCATCCTGACGATCATCACCCGCCCGCGGTACAGCTTGGCCTCCGTGACCGCACG
CATCGCCCGGTTGCGCGCACCGGACGCGCCGTACAGCCGCGCGCAC (SEQ ID NO. 161)

.....Rv17T7.seq:.....
AGCTTGCCGGGACTGCGGAACAGAAGCGGCGGTTCTACCGCGGTGTGCGGCCGGCGCGATATCGGCCTTTTTACTAA
CCGAACCCGATGTGGGCTCCGATCCGGCGCGCATGGCATCGACGGCGACGCCGATCGATGACGGCCAGGCTTACGAGC
TTGAGGGTGTGAAGTTGTGGACCACCAACGGTGTGGTAGCGACCTGCTAGTGGTTATGGCGGGGTACCGCGCAGTG
AAGGCGACCGAGGGGAATCAGCGCCTTTGTCTGTCGAGGCTGATTTCGCCCGGGATCACCCTGGAGCGGGCAACAAGT
TCATGGGACTGCGTGGCATCNAAAACGGCGTGACCCGGCTTCATCGCGTCNGGGTGCCCCAAGACAACCTTGATCGGCA
(SEQ ID NO. 162)

Clone Rv180

.....Rv180SP6.seq:.....
CTCAAGCTTGCGGATGCGGGCTGGCCAAAACCTGGCCGGGCGGGGGTTGGCTTGTTCATCAAGGGTGGGTGCGG
(SEQ ID NO. 163)
.....Rv180T7.seq:.....
CCGAAGGCCCGTTCCCGGGCGTTCAGCAAGCGATCGTCGGTTGGCCCACTGCGGGTCAATCTTTCGCGCCGCGCCGGT
CGTGAACGCCAGGTACCCGGCGGCGTACC (SEQ ID NO. 164)

Clone Rv181

.....Rv181SP6.seq:.....
ATACTCAAGCTTTTTTCTGCTCATGAAGGTTAGATGCCTGCTGCTTAAGTAATTCCTCTTTATCTGTAAAGGCTTTTT
GAAGTGCATCACCTGACCGGGCAAATAGTTCACCGGGGTGAGAAAAAGAGCAACAACCTGATTTAGGCAATTTGGCGG
TGTTGATACAGCGGGTAATAATCTTACGTGAAATATTTCCGCATCAGCCAGCGCAGAAATATTTCCAGCAAATTCAT
TCTGCAATCGGCTTGACATAACGCTGACCACGTTTATAAGCACTTGTGCGCGATAATCGTTACCCAATCTGGATAATG
CAGCCATCTGCTCATCATCCAGTTCGCAACCCAGAACACGATAATCACTTTCGGTAAGTGCAGCAGCTTACGACGGC
GACTCCCATCGGCAATTTCTATGACACCAGATACTCTTCGACCGAACGCCGGTGTCTGTTGACCA (SEQ ID NO. 165)

Clone Rv182

.....Rv182SP6.seq:.....
CTCAAGCTTGGTGCCGACATGGCCGGGCTGGAGCCCGCGTATGGCAAGGTTCCGCTCAATGTGGTTGTGATGCAGCAG
GACTACGTTTCGCTCAATCAGCTCAAACGTCACCCCGTGGCGTGCTGCGCAGCATGAAGGTCGGCGCCCGCAGCATG
TGGGCGAAGGCAACAGGTAACCTGGTCCGCGATGGGTTCGAGCCCTCATTGGGCGGTTGCGGATCGGGTTGCACCGC
GCCGGAGTGCCGGTCAACTCAACACCGCCTTCACCGATCTTTTCGTCAAAAATGGCGTCGTTCGGGGTATAC
(SEQ ID NO. 166)

.....Rv182T7.seq:.....
CCGAAGCGTGGGAAATCCTGACCGAATACCGCGACGTGCTGGACACTTTGGCCGGCGAGCTGCTGGAAAAGGAGACCC
TGCACCGACCGAGCTGGAAAGCATCTTCGCTGACGTCTAAAGCGGCGCGGGCTCACCATGTTTCGACGACTTCCGGTG
GCCGGATCCCGTCCGACAAACCGCCCATCAAGACACCGGGGAGATCGCGATCGAAACGCGCGGAACTTGGGCC
(SEQ ID NO. 167)

.....Rv183SP6.seq:.....
CGACTCGACAAGCATTCTTGACAGTTGTTTTGGCTCGGCATGGTTAGCCAAGGTTCTGCGGTCCCACCAGATCATCTT
GGTCCGGTAGCGCTCGTCCGGGTATGCTGCCGCCGGGATTCTCGCTGCTATTACTCCCCGAAAAACGCCACCGGTC
CAGCGCTGGGGCCGCGGTCCTCCCATCACAACTGAACCCCAACAGGGGACATGCTTAGCGGTAGGGCGCGCGCCA
AGGCGGCAGCAATCGCATCACTGCGCTGCGCGTCACTATTAAACCCACCGGACTTCACTTCCACGACCCCGAATGGCG
CCCGGTCAATTGATCATCTTGCACACCGCGGATAATCCGGGATTGCCAGCCCATTCGACTACCGCATGGGAGTCATCGG
CTGACCGCAGCGGTCCGATTACCCGAGCGCCCCGANTACATCTCTCCAATATCAATGGGCGCAA (SEQ ID NO. 168)

Clone Rv183

.....Rv183T7.seq:.....
GCGGTNTAGCTTCCCGTCGTACCGGCGACCGCCAGCCGAGAAGCTCGTTTTCCAGTGTTGCTGGGGATTCTCACGCT
GCTGCTGAGTGCCTGCCAGACCGCTTCCGCTTCGGGTTACAACGAGCCGCGGGGTACGATCGTGCGACGCTGAAGTT
GGTGTCTCCATGGACTTGGGGATGTGCCTGAACCGGTTACCTACGACTCCAAGCTGGCGCCGTCTCGTCCGCAGGT
CGTTGCTTGCATAGCCGGGAGGCCCGGATCCGCAATGACGGATTCCATGCCAACGCTCCGAGTTGCATGCGGATCGA
CTACGAATTGATACCCAGAACCATCGGGCGTATTACTGCCTGAAGTACCTGGTGGGGTCCGATACTGCTATCCGGC
GGTGACGACCCCGGCAAGCCGCCATCCGTGCTGCTGT (SEQ ID NO. 169)

Clone Rv184

.....Rv184SP6.seq:.....
CTCAAGCTTGGGCGTGACGGCCACCGGGCCACTCCGCACAATCTGTACCCGACCAAGATCTACACCATCGAATACGA
CGGCGTCGCCGACTTTCCGCGGTACCCGCTCAACTTTGTGTGCGACCTCAACGCCATTGCCGGCACCTACTACGTGCA
CTCCAATACTTATCCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGAC
CCAGTACTACATCATTGCGACGGAGAACCTGCCGCTGCTAAAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACT
GGCGAACCTGGTTCAACCAACTTGAAGGTGATTGTTAACCTGGGCTACGGCGACCCGGCCTATGGTTATTCC
(SEQ ID NO. 170)

.....Rv184T7.seq:.....
CGGGTGTATTGGCCACCGCGCGGGCTGTCCGGGAAATGGCGGGTCCCCGGTGGTTTTGCTGAGGAGTGCTGAACCG
TAGTCGAAGTGGGCGGCGTCAGACTCCACCCAGCGAGGCGCGGAAGCTGAATCCTCCAACCGGGTTGTCGATC
CGGACAGGTTGGGGTGCCTTTGGGGCAATGACAGGTGGCGCGGTGCGTTCCGGTCGGCCGGCGGAGGTGCTGCGTTG
GGATCGCCCGGCTGGGCATTGCGCGTGTGGCGGCGGCCGGTGGTGGGGGGCAACANGTGTCCCGGTGCGGGTGCC
GCTGCA (SEQ ID NO. 171)

Clone Rv185

.....Rv185SP6.seq:.....
NCTTGATATTGGCGTCAACGGTGTGCGCACCGGCTCCTGCAAGTTGGTAGGCCTGCAGTTTGTGCATCAGGCCGATGC
CGCGGCCCTCGTGCCACGCATGTACAGCACCGCCGCGCCCTCACGGGCGACCATCGCCAGCGCGGCGTCCAGCT
GAGGCCCGCAATCGCAGCGCGGTGACCCAAACACATCGCCGGTCAAGCACTCCGAATGCACCCGGACGACGTCGT
CACCGTCGGCGTTGGGCCCCGGCGATCTCGCCGCGGACCAGCGCGACATGTTCCACGTCCTCGTAGATGCTGGTGTAGC
CGATGGCGCGAAACTCCCATGACGAGTCGGAATCCGCGCCTCGGCGACCCGCTCAATGTGCTTCTCGTGCTTGCGCC
GCCATTGATCAAGTCAGCAATGGTGATCAGCGCCAGACCGTGCTCNTCGGCG (SEQ ID NO. 172)

.....Rv185T7.seq:.....
CATAAGGGCCGGCGTACCCGGTACCGGCCGCGGGCTACACGTCGCCGGAAGTGAAGCGCAGTAAGCCCTCAACGCG
CCACCGCTTTGGCCCCGCGCGCCCGGCTAGGCGCATCGGCGGTGGCCGTGGGGCGGCGACTGCGACCTCACCAGCGG
CTTTCGAGCTTTGTTGATCAACCGGCCAGCATGGTCGAGGATGCATTGAGACCATATTCGAAATTGGTTTCATCGG
GGGCCCCGATGCCCCCTCCAGTTGCGTGAGCAAGCAGCGGAGTCGTGCGGGATCGATGGCCACGGGGTGT
CAATGGCGGATGGTCCGTCGCCGCCGACTGGCTCTTGCGGGAGAGCCGATCTAGCACCCAGATCCGCGCACGTGGA
CCGAAACCGCGAGTAGATGTGAAAGCGT (SEQ ID NO. 173)

Clone Rv186

.....Rv186SP6.seq:.....
CGTCCTTTTCCCCAAGATAGAAAGGCAGGAGAGTGCTTCTGCATGAATATGAAGATCTGGTACCCATCCGTGATACA
TTGAGGCTGTTCCCTGGGGTCTGTACCTTCCACNAGCAAAACACGTAGCCCTTACAGGCCNNATCCTGAGCAANAT
GAACAGAAACTGAGGTTTGTAAACGCCACCTTTATGGGCAGCAACCCGATCACCGGTGGAAATAGCTCTTCAGCAC
GTCGCAATCGCGTACCAAACACATCACGCATATGATTAATTTGTTCAATTGTATAACCAACACGTTGCTCAACCCGTC
CTCGAATTTCCATATCCGGGTGCG (SEQ ID NO. 174)

Clone Rv187

.....Rv187SP6.seq:.....
CTCAAGCTTCATGTCCGTACGGCTCGGGTACGCTTCCGTCGAGTGTCGAGTGATAAATGACGACCGGGACCTCGTC
GGCATCTTCCATAGCCCGCCACACCTTCAAGTTGCTCACCGGAATCCAACCGGTAGAAGTTCGGCGAGCGCTCGGCATT
GGTCATCGGGATATGCCGCTCGGGACGGTCAGAGCCCTCGGGTCCGGCCAGCACTCCGCAGGCTTCGTGGGGTGGTC
GCGACACGCATGGGCCACCATCGCATTAC (SEQ ID NO. 175)

.....Rv187T7.seq:.....
NCGCCGCCAGCCACCACGCGGGTCGGGCGCCGGGCGCCAGGCTGCTCCGCTCGGTGATGGCAGCCACC
GCGACACCACCCGGCTGCGCTACGTCGAGCCATACCGGGCGGAGCTACATCGGCTCGGCCGCCAGTGTTCGGGCCCT
CTTTCGAGGTCGAGGTCGATACCGATTGCGCATCCGAGCCGACCCCTGGACGACAGAACCCTGCCCTACGANTGCT
TGTCGGGCGGGGCCAAAGAACAGCTTGCGATCCTGGCGGATTGGCCGGCGGGCGCTGGTCTCCAAAGAAGACGCC
TTCCGGTGCTGAT (SEQ ID NO. 176)

Clone Rv188

.....Rv188SP6.seq:.....
CGCCACGTTTCATGGGCAACAACCCGATCACCAGGTGGAAATACGCTTTCAGCACGTCGCAATCGCGTACCAAACACAT
CACGCATATGATTAATTTCGTCGAATTGTATAACCAACACGTTGCTCAACCCGTCCTCGAATTTCCATATCCGGGTGCG
GTAGTCGCGCTGCTTTCTCGGCATCTCTGATAGCCTGAGAAGAAACCCCACTAAATCCGCTGCTTCNCCTATTCTCC
AGCGCCGGG (SEQ ID NO. 177)

Clone Rv189

.....Rv189SP6.seq:.....
ATACTCAAGCTTCAACCGATTGACGCATTGTGCGAACTGACGGCGCCCGCGCATGGCCAATCCGGAAGACCATCATTG
GCCAGTGGCCGGGCGCTAACAGGTTCCAGCCCCCACCAGTGCCGCTCGAACATGCGGTGCAACCCATTTCGAGGGCCG
GCAGGGAAAGCACCCGCGGAAGCCGCAAGGGCTGCAGTTCCGCGCCCAATAGTGTCTCGTCCGCAACCAGATGCGCTCGA
AAACCGCGCCGCGCAGTCAGCGCACCCGACGCGAGGTGCGAGAGACGTCGTCAGCGCGCCACATGGGGTGCCAATCGGC
ACGGCAGGTAGGCGCGCGCAACCCGAACGCGTGGTGCATGCCACGGTCCGAGGAGGCGCAGCACCCGCCAATGCC
GAAGCCACGAAACATCGGGCGCATCCACGCTTCAACCTC (SEQ ID NO. 178)

Clone Rv18

.....Rv18T7.seq:.....
AGCTTTTGGCAGGGTCTCCTTCGAATTCGGCGTGCACCGCTATGGGTTGCAGCAGCGGCTGGCGCCGCACACCCCACT
GGCCCGGGTGTTCGCCCCGAACCCGGATCATGGTGAGCGAAAAGGAGATTGCGCTGTTTCGATGCTGGGATTTCGCCA
CCGCGAGGCCATCGACCGATTACTCGCCACCGGGGTGCGAGAGGTGCCGCGTCCCGCTCCGTCGACGTCTCCGACGA
TCCATCCGGCTTCGCGCGTCGGGTGGCGGTAGCCGTCGATGAAATCGCTGCCGGCCGCTACCACAAGGTGATTCGTGTC
CCGTTGTGTCGAAGTGCCTTTCGCGATCGACTTTCGTTGACCTACCGGCTGGGGCGTCGGCACAACACCCCGGTGAG
GTCGTTTTTGTGTCAGTTGGCGGAATCCGTGCTCTGGGTTACAGCCGAATCGTCAC (SEQ ID NO. 179)

Clone Rv190

.....Rv190SP6.seq:.....
ATACTCAAGCTTTGTCACACCACTGTTTCCACGAGCGCTCCATCCGGCGAGTGGATACTCCAGCAGGTAGCAGGT
CGCCACCACGCTGGTCACTGCGCGTTCACTCGCTTGGCGCGCTGCAGCAGCCAGTCCGGGAAATAGCTGCCCTGGCG
CAGCTTGGGGATCGCGACTTCTATGTTGCGGCACGGGTGTGCAATACAGGTGCGCGTAGCCGTTGCGCTGATTGGA
CCGCTCATCGCTGCGTTGCGGTAAGCCCGCCCGCACAGGGCGTCGGCTTCAGCCCCATCAAGGCGCGATGAACGT
CGAGAGCAGCCCGCGCAGCAGATCCGGGTCGCTGTGCGAGTTGGTCAGCCAGAACCTGCTCGGTGT (SEQ ID NO. 180)

.....Rv190T7.seq:.....
CCTTAAGCCCCGAGGGCCCGGCACGCGCGGTACCGCCAGGTGCCCCAACAGATCGTCGATGTTGCGCTCGTCCGCC
TCGCGCACGTGGTCTGTACCAAGTCAACGTTAACCGCGCCGCACATGTCCTGCGGCCGGGCAAAAACGTGAAAAACGA
GCGGGCGACTGCAATGTCATGACACCGACGGCCCGCGATGGGCCAGGGTCTGGCAGATTGATCTGTGCGGCCAGTG
CCAGCAGCGTCGCTCGTCATACGGCCGGCGACGAGTTGAACCGACATGGGCAGGCCGTCGCCGTCGAAGTCCACG
GCACCACGGCCGCGGGTGGCCGGTCAGATTCCAGACTTGAAGTACGGAACCCGCTGCACCACCAGCAGCAACGTCG
AAACTGCACCCCGCGGTTGGTAGGCGCCGATGCGGGACGGGCGGTGCGGGCGCCTGGCGTCACAACTACGTCGACAT
CGTCGAAGATCGACTGGATCGGCTGCTCACACCACTCGGCGGCCGAGGCCGCCATCCGCGTC (SEQ ID NO. 181)

Clone Rv191

.....Rv191SP6.seq:.....
AGCTTTTTCGAGCGTCGCGCGGGGCGAGCTTCGCGGCAATTCTACTAGCGAGAAGTCTGGCCCGATACGGATCTGACCG
AAGTCGCTGCGGTGCAGCCACCCCTATTGGCGATGGCGCGCAGATGGCGCCTGGACCGATCTTGTGCGCGTTGCGG
ACGGCGACGCGGTGGGTGGTCAAGTCCGGTCTACGCTTGGGCTTTGCGGACGGTCCGACGCTGGTCGCGGTTGCGC
CGCGAAAGCGGGTGGGTGCCATCAGGAATGCCTACCGCCGCGGCACTGCACGGCCAGTGCCCGCGGATGTCA
GCCATCGGGACATCATGCTCGGTTCTACTCTCGACAGTCGGCGGAACAGCTCGATTCCCGGACCGCCAGCGCA

TTGGTGATGGAATCGGCGAACTTGGCCACCCGCTGGGTGTTGACATCCTCGACGGTGGGCAATTGCCCCGGTAACGT
TTGCCGCCT. (SEQ ID NO. 182)

.....:Rv191T7.seq:.....
CGGTCCGACCCTGTTGACGGCTACCTGAATCAACCCGATGCCACCGCCGCGGCTTCGACGCCGACAGCTGGTACCG
CACC GGCGACGTCGCGGTGGTTCGACGGCAGTGGGATGCACCGCATCGTGGGACGGAGTGGTTCGACTTGATCAAGTC
GGGTGGATACCGGGTCGGCGCCGGTGAATTGAAACGGTGCTGCTCGGGCATCCGGACGTGGCGGAGGCGGCAGTCGT
CGGGGTGCCCGACGATGATCTAGGCCAGCGGATCGTTGCCTACGTAGTCGGCTCAGCGAATGTCGATGCGGACGGGCT
TATCAACTTTGTTGCCCAACAACTTTTCGGTGACAAAGCGCCGCGAGGTGCGTATCGTANATGCGCTGCCGCGCAA
CGCCTTGGGGAAAGTGCTCCAGAACATTGCTGTCAGAAGCTGANCTACCGGAATTATCGTGTTACGCTGGA
(SEQ ID NO. 183)

Clone Rv192

.....:Rv192SP6.seq:.....
ATACTCAAGCTTGCCGAAGTTCCGATGGGTGCGCGCCGGCAGGCCAGCGAAGTCGTACCGTGCCCGTGTCTTGGCT
TCGGATCTATCCTCGTTCATGACGGGCACCGTGTGGACGTGACTGGCGGCCGGTCCATATGACACCGAGATCATTGC
CACGGTACGGCAATTTCGTCAGAAGGAAATCTTTCCCAATGCACCGGCCCTCGAACGTGGCAACAGCTACCCGCAAGA
AATCGTCGATCGGCTGGGTGTTATTGGCTTGCTCGGTGCGCGGCTGCAAGGGTATCGACACCACCGAGTTTATTCTCG
GGCGTGCCGGCGCATTCGAGCTGGCGGTGCGCGCTGCCAGCACCGTCATAGGTACTTGACGATGGTCCACGTCGGAC
GAGCGCTCCACGTCGCTGCCGAACGGTATGCATGGCGGCTACGATTCTC (SEQ ID NO. 184)

.....:Rv192T7.seq:.....
CGGTGTCGGCACCGCGTCTGCGAGTTGGTAGGCCTGCGAGTTTGTGCATCAGGCCGATGCCGCGGCCCTCGTGGCCAC
GCATGTACAGCACCGCGCGCCCTCACGGGCGACCATCGCCAGCGCGGCGTCCAGCTGAGGCCCGCAATCGCAGC
GGCGTGACCCAAACACATCGCCGGTCAAGCACTCCGAATGCACCGGGACAGCACGTCGTACCGTCGGCGTTGGGCC
CGGCGATCTCGCCGCGGACAGCGCGACATGTTCCACGTCCTCGTAGATGCTGGTGTAGCCGATGGCGCGAACTCCC
CATGACGAGTCGGAATCCGCGCCTCGGCGACCCGCTCAATGTGCTTCTCGTGCTTGCGCCGCCATTGATCAAGTCAG
CAATGGTGATCAGCGCCAGACCGTGCTCATCGGCGCAACACCGCAATTCATCGGTGTTGCGCCATCGAGCCCTCATCTT
TTTGGCTGACGATCTCGCAAATCGCCCCCGGGGTGCGAGCCGGCAT (SEQ ID NO. 185)

Clone Rv193

.....:Rv193SP6.seq:.....
ATACTCAAGCTTTGGGTGAAAGCCGATCACCGGAAGCCGATGATCAGCCACGTTTCGCGCCGCCCGGCATACGGCGG
CGTACCGATCTCCGCGTCATACACCCGCGGGTAATCGCCGACGGTGCCGGTTCGCGAGCCGAAGGTGACGACGCTGAT
TGAATCGAGTTCCAGGTCCAGCGGGTGGCGCAGCAACGGCGGAGCTCAACGACGTCATCAGGTTGTCGCTTTCTAC
GGTCACCGACCCGGTGACCGTNCCTCGCCCGGTGCGCTCGGCCGATAAGTTGCACCGCCACCACCGCGACACCGTCTTG
CACGGGACCCACCCCGGATCCGTTGTTGGCC (SEQ ID NO. 186)

.....:Rv193T7.seq:.....
AGCTTGCTGGCATCCGCTCCAGTAGCGCCCCGCGGTGGCTTCAGCGCCCGCAGATGCTCCATGAGCCGGCCGGTTCG
AGTCGGCGCCGGCGTTACCGCCACCCGCCAGGAGTGGCGGCCAGCATCTCCGCCCTCAGCGATTGCGCGATCACAG
AGAGAATATACGTCTCATATTGTTGGAGGTGCTCGCAGGCAATCGGTGATGACGGATTTGATGGCATCGAGCTGTG
CTTCGGCGTAGCCCTCCAGCACGTCGGTATCGCTGTGGCGGTCCACGACGACCGCACCGGCGCGGCGGACAGCCGTCG
GGTTGGACGNTGTGCGCGATCAGTCCGGCCAGTCCGCCCTCGGGATCAGCGGC (SEQ ID NO. 187)

Clone Rv194

.....:Rv194SP6.seq:.....
ATACTCAAGCTTGCTGCGAGCTTCCTATGACTGCTCCGAAACCTGGGGGTGTGCCTGCTGTGTATGCACGGCATAACGG
ACATCCTTCCCCTGAGACCCGCGGTGCAACAGCCACGTGTCCATCATCAGGGGTCAACCCCGGCCAAGGGCGACGGC
ACGCCAAGTTGCGCGACCGTTAACCTAGTGCTGTAGCTTCATTTGCTGCGAGCAAAACAGCTGGTGGCCGCTTAGGA
ACTGAATTGAAACTCAACCGATTTGGTGCCGCGTAGGTGTCTGGCTGCGGGTGCCTGGTGTGTCGCGTGTGGT
AACNACNACAATGTGACCGGGGGAGGTGCAACCACTGGCCAGGCGTCGGCGAAGGTGATTGCGGGGGGAAGAAGAAC
TCAAAGCCAGTGGGTGACGCGCAGGCCAACGC (SEQ ID NO. 188)

.....:Rv194T7.seq:.....
AGCTTGACGGGAGACGGACACATTGCGAACATTGATGACAAAATAGAAATCATTGATGGTTTGAGTCACCAGGCCGA
TCAAGCCTTTCGCCGAGCCAAATTCGAATCAAGAGGCCCAAGCCCGTACCAATCAGCCCGGCAACGAGGGATTCCGTCA
TTATCAGCCAAAATAACTGCTCTCGGGTTACACCCAAACAGCGCAATATGGCGAAAAACGGTCGCGGTTGACCGACAT
TAAATGTCACGGTATTGTAGATTAATAAGATACCCACCAACAAGGCAATCAAATGAGAGCGGTTAAATTGACCGTAA

AAGCGTCCGTCACTCTGTTGACGGTGTCCCGTTGGGTATCCGACGTTTCCATACGCACACCGGCCGGCAGTCTTTGTT
GGATGCGTGTGTCAGTGGCCTCATCTTTGATGATCAAATCGATGTGGCTCAGTCTTCCGGGCA (SEQ ID NO. 189)

Clone Rv195

.....Rv195SP6.seq:.....

ATACTCAAGCTTCGGCTCAGGCGGCGCTGCTGGTAAAGTCGCTGACCGGTGCAGGTTTCGACAATGTGGTGCCGGTTC
GGCGGCTACGTGCCATCGAGACACTGGCGCAGGCTATCGCACCCGTTATCGGCTACGAGCAAATCGCGGTATGCGTTC
TTGAGCATGAGTCGGCGACCGTCGTATGGTCGACACCCACGACGGAAGACGCAGATCGCCGTCAAGCATGTGTGCC
GCGGATTATCAGGACTGACCTCCTGGCTGACCGGCATGTTGGTCGCGATGCCTGGCGCCCGGGCGCGTGGTCGTGG
TCCGCTCGGATAGCGAGGTACGCAATTTCNCNTGGCAGCTCAAAGGGTCTTCCCGGTGCCGGTCTTTCGCGAAACNA
AGGCNCAGGTTA (SEQ ID NO. 190)

.....Rv195T7.seq:.....

TGATCGCGCATCACCTGCTTCATAAACTGGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCAACATGAGCCAGCCTCTCG
TCGGCGGTTCGGGTGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCTGAAACCAGCTTCCATATCCCGCG
ACGAACGACGCCAGTCCGCTACGTAACCCCTCCGCGACTGTCATGGACAACAGCGCGTTCACCCGACCGGGCCCG
GGTGTGGGTGTTTCGGCGACCGGCAGCCAGGTGGTCCCACTGCCGACGGCGCCGCGAGCCGTTACCCGACCCAGGC
CGCCGAGCAAGTCCGCGCGATCGCATACTCAACCGGTTGCGGTACTGCAGGTTAGCTGGCGTACTCCTCGTCGCGC
TCGGCGAGGTCTTGCTCCAGCACGTGCGANACGGCAG (SEQ ID NO. 191)

Clone Rv196

.....Rv196SP6.seq:.....

CAAAGCGCAACTGCTCGCGGCAGCCACGACGTGCTGCGTCGGATTGCCGGCGGCGAAATCAATTCCAGGCAGCTCC
CGGACAATGCGGCTCTGCTGGCCCGCAACGAAGGACTCGAGGTACCCCGGTGCCCGGGTTCGTGGTGACCTGCCGA
TCGCAAGGTTGGCCCAACAACCGCCGCTTGATGCCCGGTTCGGCAAGCCCGGAGTTGCCAAACCCAGCGTGATCAGG
CTCGGCTCGCGAGTTCCGGGAAGAAGTGGCTCCGCTGATCACCTACCATCCGCCAGGATCTGCGTGTCTTACCACG
CCCGCCAAGGAGGTTGTTGTGGTCTATCGACCGN (SEQ ID NO. 192)

.....Rv196T7.seq:.....

CCGGAAGCCGCATGATCAGCCAAGTTTCGCGCGCCCGGCATACGGCGGCGTACCGATCTCCGCGTCATACACCCGCG
GGTAATCGCCGACGGTGCCGGTTCGCGAGCCGAAGGTGACGACGCTGATTGAATCGAGTTCCAGGTCCAGCGGGTGGC
GCAGCAACGGCGCGAGCTCAACGACGTCATCAGGTTGTGCTTTCTACGGTCACCGACCCGGTGACCGTNGTCGCC
GGTGCGCTCGGCCGAAAANTTGCACCGCCACCGCGAAACCGTCTTGACNCCGGAAGCCACCCCGATCCGTTGT
TGGGCCAGGTTATTGGGT (SEQ ID NO. 193)

Clone Rv19

.....Rv19SP6.seq:.....

CCGGAACCGCCGACGGCACGGTATAACGCCTCCGCATATGGGTGACAAACAGCGGGTCGGACTTCTGGGCTTCTAGC
GTTTCGCGCNGTCGCGACAAACAGCGCGGTGCAACCGACACTCGTTGTGATGTCCTAGCTATCAGGTTCCGTACGCACC
CAATCGAGTCTAGCGCGGTAGNTCAGCCCCGATCTCCANGTCCGCCGAGCCAGGCGC (SEQ ID NO. 194)

.....Rv19T7.seq:.....

CTGGTTTATGTCCCGTTGAAGTTCCATCACCCGATGTGGCGGGAGCACTGCCAGGTGATCTCAACTACCACATCCGG
CCGTGGCGGTTGCGCGCCCCGGGGGTCGGCGCGAACTCGACGAGGCGGTGCGAGAAATCGCCAGCACCCCGCTGAAC
CGCGACCACCCGCTGTGGGAGATGTACTTCGTTGAGGGGCTTGCCAACCACCGGATCGCGGTGGTTGCC

(SEQ ID NO. 195)

Clone Rv1

.....Rv1SP6D2.seq:.....

CCGAGCAGTTGGGAATCGCTCTGCANCAAACCAATATTCTGCGCGACGTGCGCGACGAGCTGGACCGATTAGGCGTA
CGCTCCGNTGGACGACACCGGGGCACTCGATGACCCCGACGCTACGCTCGCAGGATATTGTTCCCGGACCCCTC
TCTAG (SEQ ID NO. 196)

.....Rv1T7.seq:.....

TATATAACTCAAGCTTGCCGACGCCAACGCTCGCGCGATGTTGTTAGCCCGACCCGGCTCTTACATGGCACCGGTG
CCCCACAGTCAGCCTGTGACGTCCTGCACCGGACTCTTACATAGAATGTGGATTGCCGGATTGGGGATGTCCGGC
ATCGCTCAATCTGTAGTCCGCGTTGTCCCGGAGGGCCATGTGGATGGGGGAAGGATCCGTGGCGTCCGGGATCACC
ATGGGG (SEQ ID NO. 197)

Clone Rv201

:::Rv201SP6.seq:::

ATACTCAAGCTTGCCGAAGTTCCGATGGGTCGCGCCGGCAGCCCAACGAAATCGCTAGCGTGGCCGTGTTCTTGGCT
TCGGATCTATCTCGTACATGACCGGCACCGTGTGGACGTGACTGGCGGCCGGTTCATATGACACCGAGATCATTCG
CACGGTACGGAAATTCGTCCAGAAGGAAATCTTCCCAATGCACCGGCCCTCGAACGTGGCAACAGCTACCCGCAAGA
AATCGTCAATCGGCTGGGTGTTATTGGCTTGCTCGGTGCGCGGCTGCGAGGGTTTCTACACCACCGAGTTCATTCTCG
GGCGTGCCGGCGCATTCGAATGGCGGTGCGCGCTG (SEQ ID NO. 198)

:::Rv201T7.seq:::

GCACCGGCTCCTGCAGTTGGTAGGCCTGCAGTTTGTGCATCAGGCCGATGCCGCGGCCCTCGTGGCCACGCATGTAC
AGCACCACGCCGCGCCCTCACGGGCGACCATCGCCAGCGCGGCGTCCAGCTGAGGCCGCAATCGCAGCGCGCTGAC
CCAAACACATCGCCGGTCAAGCACTCCGAATGCACCGGACAGCAGCTTTCACCGTGGCGTTGGGCGCGGCGATC
TCGCCGCGGACCAACGCGACATGTTCCACGTCCTCGTAGATGCTGGTGTAGCCGATGGCGCGAACTCCCCANGACAA
GTCGGAATCCGCGCCTCGGCGAACCCTCAATGTGCCTCTCGTGCTTGCGCCGCCATTC (SEQ ID NO. 199)

Clone Rv204

:::Rv204SP6.seq:::

TGGTCCGTGTGCGCATACCAATACAACGCGCGGGCACCTGACGCGGCGGCCGCAACCAATCGGTGGCCATCGCCATC
TTCTGCTACCCGGTCAACGGACGCACCTTCTCCTGGCCGACGTAGTGCGCCACCCGCCCGCTTGGTCCCATCGAT
CCGGTCAAC (SEQ ID NO. 200)

Clone Rv205

:::Rv205SP6.seq:::

GGCGTGTGGCCACCGGGGCCACTCCGCACAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCGCC
GACTTCCGCGGTACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAACCTAC
TTCATCTGACGCGGAACAAATTGACGCGAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACTAC
ATCATTCGACGCGGAGAACCTGCCGCTGCTAAAGCCACTGGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCT
GGTTCAACCAAACTTGAAGGTGATTGTTTACCTGGGCTACGGCGACCCGGCCTATGGTTATTGACCTCCCCGCCCAA
(SEQ ID NO. 201)

:::Rv205T7.seq:::

CGTCCGTGNCCCTCAANCGCGTGNNGCCGAAGCGGCTGGTTACGACTCCCTGTTTGTGATGGACACTTCTACCAACT
GCCCATGTTGGGGACGCCCGATGCTGGAGGCCTACACGGCCCTTGGTGGCTGGCCACGGCAGCCGACCGANCG
GCTGCAACTGGGCGCGTGGTGACCGGAATACCTACCGCAGCCCGACCCCTGCTGGCAAAGATCATCAACCGCTCGA
CGTGTTAGCGCCGGTCGAGCGATCCTCGGCATTGGAGCCGGTTGGTTTGGAGCTGGAAACACCGCCAGCTCGGCTTCG
AGTTCGGCACTTTCAGTGACCGGTTCAACCGGCTCGAAGAGGCGCTACAGATCCTCCAGCCAATGGTCAAGGGTGAGC
GCCAACGTTTTTCGGCGATTGGTACACCACCGAATC (SEQ ID NO. 202)

Clone Rv207

:::Rv207SP6.seq:::

CCGCTTCCGTGTAACCGAGCANNGCAGCGANCTGGCGAGGAAGCAAAGAAGAACTGTTCTGTCAGATAGCTCTTACG
CTCAGCGCAAGAAGAAATATCCACCGTGGGAAAACTCCAGGTAGAGGTACACACGCGGATAGCCAATTCAGAGTAAT
AACTGTGATAATCAACCCTCATCAATGATGACGAACTATCCCCGATATCAGGTACATGACGAAGGGAAAGAGAAG
GAAATCAACTGTGACAACTGCCCTCAAATTTGGCTTCTTAAAAATTACAGTTCAAAAAGTATGAGAAAATCCATGC
AGGCTGAAGGAAACAGCAAACTGTGACAAATTACCCTCAGTAGGTGAGAACAAATGTGACGAACCNCCCTCAAATCT
GTGACAGATAACCCCTCAGACTATCCTGTCGTGATGGAAGTATATCGCGGAAGGAAATACGATNTGAGTCGTCTGGC
GGCCTTTCTTTTCTCAATGTATGAGAGCG (SEQ ID NO. 203)

Clone Rv209

:::Rv209SP6.seq:::

TGACACCCAACAGAGGGCACTTAAGATGGCAATGCGGCCGCTACCTGCACGTTTTCGCGATGTCAGAGGATGCCGAG
GGAGAACAATGCGAGCACGGCCGCTGACNTTGTCAACGCTTTGGCGCGGCTGACATTGGTGGTGGTGGCGGCTGCN
AGGCCCGANTCNAGCCGAAGCATATAGCGCGGCCGACCGCATTTCTGCTCGACCGCAAGCGCGACCTCAGCCGCAGC
CGGTGGAGCTACTGCTGCGCGCCATCACGCC (SEQ ID NO. 204)

:::Rv209T7.seq:::

ACGGGCGACGCTGAGGTGGGCGCGGCTATTATGCTGTGCTCCACGTCCAGCGACGCACTGCGCCAGACGGCCCGC
CAACTAGCCACCTGGGTGGAAGAACACCAGGACTGCGTGGCGGCTCGGATCTGGCCTACACGCTGGCGCGTGGCCGC
GCGCACCGGCCGCTGCGCACCGCGGTGGTTGCGCCAACCTGCCGAGCTCGTCGAGGGTTGCGCGAGGTGGCCGAC

GGTGACCCCTCTATGACGCGGCGGTGGGACACTGTGATCTAAGACCGGTCTGGGTCTTCTCCGGGCAAGGGTCTCAGT
GGGCGGCGATGGGCACCCAATTGCTCGCCAGCGAACAGTGTTCCGCGGCCACCATCG (SEQ ID NO. 205)

Clone Rv20

::::::::::::Rv20SP6.seq::::::::::::
ATACTCAAGCTTCGCGAGATCCGGATGGCACTCACGCTGGACAAGACCTTCACAAAATCTGAAATCCTGACCCGATAC
TTGAACCTGGTCTCGTTCGGCAATAACTCGTTCGGCGGTGCAGGACGCGGCGCAAACGTACTTCGGCATCAACGCGTCC
GACCTGAATTGGCAGCAAGCGGCGCTGCTGGCCGGCATGGTGCAATCGACCAGCACGCTCAACCCGTACACCAACCCC
GACGGCGCGCTGGCCCGGCGGAACGTGGTCTCGACACCATGATCNAAAATCTCCCGGGGAGGCGGAGGCGTTGCGTG
CCGCCCAGGGCGAACCGCTGGGGGTTCTGCCGCGACCCAATGATTGCCGCGCGGTGCATCGCGGGCGGCGACCGCCA
TTCTTCTGCGAATACGTCCAGGAGTACTGTCTCGGGG (SEQ ID NO. 206)

::::::::::::Rv20T7.seq::::::::::::
AGCTTATGTGGCCGCCACCTACCTTATCTAGCCTAGCTAACTAAATCCAGTGCCGACAGTGCGCGGCTGGCCACCCA
GCATGAGGTTATGACCACGGCATATGCCAGCGCGCTGGCGGCGATGCCGACGCTGACCGAGTTGGCCGCTAATCACAC
CAGCCATGCGGTGTTGCTGGGAACGAATTTCTTTGGAATCAATACGATCCCGATCGCGCTCAATGAGGCCGACTATGC
GCGGATGTGGATTGAGGCGGCCACACGATGAGTATCTATGAGGGCACCTCCGATGCGGCGCTGGCGTCNGCACCGBA
AACCACACCGGCTCCGGTACTGTTCAACGGCGGTGCTGGCGTTTGCCAGCGCCTGCCGGCGATCTC (SEQ ID NO. 207)

Clone Rv214

::::::::::::Rv214SP6.seq::::::::::::
ATACTCAAGCTTGCCACCCATGCCGAGCAAGGTGCACTCAGCGATGACGAATTGTTCTTCTCGCGGTGTTGCTGCTG
GTTGCGGGCTATGAGAGCACTGCTCATATGATTAGCACNTTGTCTTCTGACGCTGGCCGACTATCCAGATCAGCTGACA
CTCCTTGCGCAGCAACCAGACCTGATCCCGTGGCGATCGAGGAGCACCTCCGCTTTATATCGCAATCCAAAACATCT
GCCGCACAACGCGCGTCACTATTGCGTGGTCAAGCGGTCAATCCCGGGA (SEQ ID NO. 208)

::::::::::::Rv214T7.seq::::::::::::
CCGGGGTAGAACGATGCGATCTGGGCCATGTCGACATCGGTGGTACAGGTAAACCGCGCCGTGTGCGCGGTCTCGGAG
ATCAGAACGTGGTTCGAGTTGACACCGCGGGCTTTCAGCCAGTCGCGATAATCGGCGAAGTCGGCGCCTGCCGCCCA
ACTAGCGCGACCTCGCCACCTAGCACACCGATGGCGAAGGCCATGTTTCCGGCCACGCCGCCGCGGTGCATCATCAAC
TC (SEQ ID NO. 209)

Clone Rv215

::::::::::::Rv215SP6.seq::::::::::::
ATACTCAAGCTTGGCGGCAACGCCACTACCGGGCTCACCAGGTCTGTGCCGCCACCGCCGGCGCCGAAAGCACCATC
AGGTCGTAGTTGTCTGGACGTTTCGACACCGTAAGCGAACAATGCCGCCGCCATGCTGTGCCCGAGCAGATGCGC
TTGCACCCGGGATATTCCCGGTGGCGATCCCAACGAGGGGTGTCGAAGTCAGCGGTGTATCTGAGATGTCTCTACTA
TCATCCGTTTGGCACCCGAGCGGCGATGCCCGGGGGGTCAAC (SEQ ID NO. 210)

::::::::::::Rv215T7.seq::::::::::::
GTCGACGGCATCAAGGTCCGCAGTGATGGTGTTTATCTCACCCAGGAAGGCGTGAAGTGGCTGATACCGTGGCTTGAG
GATTCCGTTGCGGGTCGCCAGTTAATCCGCCGTGTGCTCCGGATGAGCGCGACGGTAACCTGGAATTGTGCTGTGTGC
TGGCTGTGTCGTTGTGATGAGCCTGTCTAAGTGGTGCGTAACCGTTTGACGAGCCGCGGCCTCGCTGCAAACATTGAA
GCCCGCACGTCTGGGTTTGTATTTACACAACGAGGGCGCTCCCCGATCTGGCGCGCGCAACGAGGTGCNCACTATCCA
TTCGAGGTGAAGTGGACTCCTTGATGCTCATGCCGTTGCGGTTTGTGTC (SEQ ID NO. 211)

Clone Rv217

::::::::::::Rv217SP6.seq::::::::::::
ATACTCAAGCTTGCCTTCGATGAAGTAGTCGTGGTCAGCGCCGCTCTTCGAGCTCCTTGCGGATGCCAGCAAGGA
GTCATCGCCGCCGAGCTTGGCCAGGATCTTGTCCGCTGCTCGACCGCGCTTCTTACGATGCGGGCCCGGATCGTAGTTCTTGTA
GACACGATGACCGAAACCATCAATTTGACCCCGGCTCGCGGTTCTTGACCTTGCGTTACAAACTCGCTGACGTGCGT
CGCCGCTGTGCGGAATGCCCTC (SEQ ID NO. 212)

::::::::::::Rv217T7.seq::::::::::::
NGTCAAGCCGAGCATGCGCGAGGNAACGACGAACCAACGCCATGGTGGTTGGCGCCGTGAGAGGTGCGCGGTGCG
CCACAACGGGAAGATCGCCTTGAGCGTCGCTCGACCGCGCTCGAGTTGGGTACATAACGAAGTAGCTGATGCCGATC
ATGTGACGTTTCCGTGCGATCAGCGTGACGCGGCGACCCACTCGACGAGGTCTCGGTGCCGCCGCGGCCAGGGCACC
AGCAGTGACGATTCCAGGCGCGGTGCGG (SEQ ID NO. 213)

Clone Rv218

.....Rv218SP6.seq.....
CGATAATCGCTTCCGGTAAGTGCAGCAGCTTTACGACGGCGACTCCCATCGGCAATTTCTATGACACCAGATACTCTT
CGACCGAACGCGCGGTGTCTGTTGACCAAGTCAGTAGAAAAGAAGGGATGAGATCTCCCCGTGCGTCTCAGTAAGCAGC
TCCTGGTGCAGTTCATTACCTGACCATACCCGAGAGGTCTTCTCAACACTATCACCCCGAGCACTTCTAGAGTAAAC
TTCCCATCCCGACCACATATAGGCTAAGGTAATGGGCATTACCGCGAGCCATTACTCCTACGCGCGCAATTAACGAAT
CCACCATCGGGGCGCGTGGTGTCTN (SEQ ID NO. 214)

Clone Rv219

.....Rv219SP6.seq.....
NAATACTCAAGCTTTCTCGTGATTACCAACCGTGTAATTTGGGATGGGCAAAAAGGCGAATCACCGCGTGGCCACAAA
CGCCGGGAGGGACAACTCTCGGGCGGCTAGGGCTTCTCGCGGAAGGCCCGAACGTACGGCGTTTCAACACGTCGCGTC
GCCCTCCGACCGCGAACATTCTGGGGATGGCAGCAACCTGGTATCACCTGGCCGGGCAATGATCTGCAGCGTCGCCGC
GGGTAGTGNCCGCGCGGGCGGCTAC (SEQ ID NO. 215)

.....Rv219T7.seq.....
CCAAGTAGAGCATCGGGACATACGGAGTCAACTACCCGGCCAAACGGTGATTTCTTGGCCGCGCTGACGGCGCGAAGC
ACGCCAGCGACCACATTCAGCAGATGGCCAGCGCGTGCCGGGCCACGATGTTGGTGCTCGGCGGCTACTCCAGGGTG
CGGCCGTGATCGACATCGTCACCGCCGACCACTGCCGGTCTCGGGTTCACGCAGCCGTTGCCGCCGCGAGCGGACG
ATCACATCGCCGCGATCGCCCTGTTGCGGAATCCCTCGGGGCGCGCTGGCGGGCTGATGATCGCCCTGACCCCTCAA
TTCGGGTCCAAGA (SEQ ID NO. 216)

Clone Rv21

.....Rv21SP6.seq.....
ATACTCAAGCTTGCTGCAGCTTCTGTGACTGCTCCCGAAACCTGGGGGTGTGCCTGCTGTGTATGCACGGCATAACGG
ACATCCTTCCCTTGAGACCCGCGGTGGAACCGCCACGTGTCCATCATCAGGGGTCAACCCCGGCCAAGGGCGACGGC
ACGCCAAGTTGCGCGACCGTTAACCTAGTGCTGTTAGCTTCATTTGCTGCGAGCAAAACAGCTGGTCGGCCGTTAGGA
ACTGAATTGAAACTCAACCGATTGTTGTCGCCCGGTAAGTGCTGCTGGCTGCCGGTGCGTGGTGT
(SEQ ID NO. 217)

.....Rv21T7.seq.....
AGCTTGCGCGCGTGGCGATCGCGGTTCAAGGCGCGCTCTTCGAGCACAAACGAGCGAAGACAGCTCGGCGACGGAGCC
TTTATCGACATCCGTTGCGGCTGGCTGACCGGCGCGGAAGAACTGCTGGACGCGTGTGTGTCGACGGTGCCGTGGCGA
GCCGAGCGCGTCAAGTGTACGACCGGTTGTCGATGTGCCGCGGCTGGTGAGTTTTACGACCTGACCATCGAAGAT
CCGCCGATCCGACGCTGGCGCGGATGCGCC (SEQ ID NO. 218)

Clone Rv220

.....Rv220SP6.seq.....
AATACTCAAGCTTGCGCACGACGACGTCGAGTGGCGCTTGCACTGACTTGCGGACCTCAAAGGCCACCGGTACCC
CGCCGCGCGCAAGCCAAGGACNACNACGGCCTTGCCGGATAGTGCGCCAGGCGTTGCGCCAAGTGGCGTCCAGCGT
CGCCACGATCGTCAAAGAGCTTCATCTGCCAGTGTGTGCCATCTCATGGCTCCAAATATGGAATTAGGTCCCTGGG
CCGACTGACGACAGTCCCTCAGCGACCGGATTGCGCATCCCGCCTGTACGCTGCTCCGCAATCCCGGGCTTGGCTC
CGCGAAGCGAACTCGGCGGCGCTACGGTGGTGGCTCACTTCGGCCGTGC (SEQ ID NO. 219)

.....Rv220T7.seq.....
GGTGGTGCGGTCCACCTTCGCGGCGGCGCGCATATGCCTTGCTGGTCTTGCTCATTTGATATCCAATCTATGGGT
CGTGTTACTCAGCGGGCCGAAGCTGGCCCTCCACGGGTAGGGCCCTATTTCGACGGTGATGCCATCGACCGAGCGG
TACCGCGGATGATCTTGCCGCGAGCGTCGACGTCGTTGGCGTTGAGGTCCGTCTTCTGGTCTCGGCGATTTGCGCGA
CTTGATCCCAGGTGACTTTGGCGACCTTGGTCTTGTGCGGCTCCGCCGAACCTTCGCCACACCAGCGGCCCTTAAGCA
GCAGCTTGCGGCGGGCGGCGTCTTCAGCGTGAAAGTGAAGTACGGTCTTCATAAACGGTGATCTCCACCGGGATGA
CGTTGCCGCGCTGGTCTCCGTCGCGGCGTGTACGCCTTGCAAGAACTCATGATGTTGACCCGTGCTGACCGAAGCG
GGGCGCACTGGCGGGG (SEQ ID NO. 220)

Clone Rv221

.....Rv221SP6.seq.....
ATACTCAAGCTTTTCGACCCGAAGCGGCGGTGCCCTCCTCGTTCCGCTGCCCGGTCTGCTCGATCGGTTTCGGGGT
CGCCGCGCTAGGCCCAATTGCCCGGCTCCTCCTCGGGCGGTTCCACAACCCGATCGTCGCGGGCTAGGTTCAAGCC
ATGCCGGTAAACCCAGGACGCCAGTGCTGATCGGCTATGGACAGGTCAACCAACGAGGCGACATCGACGCCNAAAAAT

CAGTCCATCGAACCCGTCGACCTGATGGCCNCCGGGCCCGGAAAGCCGCCGAGTCCACCGTGCTCGAAGCGGTGGAT
TCCATCCGTGTGGTGCACATGCTGTCGGCGCATTAACCGGAATTCGCGGCGTCTCCTCGGC (SEQ ID NO. 221)

::::::::::Rv221T7.seq::::::::::
NCCTGGTTCATGAAGTGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCAACATGAGCCAGCCTCTCGTCGGCGGTGCGG
TGCAGGTGCTCGGGCAGCTCGGCCGCGACGCCGCTGACCCTGAAACCAGCTTCCATATCCCGCGACGAACGACGCC
AGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCTTCTCCACCGACCGGGGCCGGGTGTTGGGGTG
TTCGGCAACGGCAACCAAGTTGGTCCACACTGCCGACGGGCGCCGCAATCCGTTACCGAACCAGGCGCCNAAACA
ATTCCGCCCCGATCCCATAT (SEQ ID NO. 222)

Clone Rv222

::::::::::Rv222SP6.seq::::::::::
ATACTCAAGCTTGTGCGGATCAATCTCGAGGGCATCCACGCACGAAAAGTAACTCTATCAAGCTTTTTGACGACACC
CACGGACGCCCCATATATGTTGCGGTGGGCAAGAAGGTCCCTACCTGGAACGTTTGGTGGCCGGCGACACCGGTGAG
CCCACGCCGCGAGCGGGCCAACCTCAGCGACTCGATTACCCCGACGAAGTACTCTACAGGTGGCCGGAAGAGCTCTTT
GCCACACCGCAACAGGGACGGACTTTGGGCTTGGACCCAGAAACCGGCCACGAAATCTTGGCAGGGGAAGGCCGGTT
TGGGCTTATGTTACCTATATCTGCCGGAACCTGCGGCTGATGCGGCCGCGGCGCTCAGGGAN (SEQ ID NO. 223)

::::::::::Rv222T7.seq::::::::::
AGCAGCTAGCCGCGCTCGCCGCGCTGGTGGTGGCTGCTGCTCGCAGCCGGATGCACCAACGTGGTGCAGGGGACCG
CCGTGGCTGCCGACAAATCCGGACCACTGCATCAGGATCCGATACCGGTTTCAGCGCTTGAAGGGCTGCTTCTCGACT
TGAGCCAGATCAATGCCGCGCTGGGTGCGACATCGATGAAGGTGTGGTTCAACGCCAAGGCAATGTGGGACTGGAGCA
AGAGCGTGGCCGACAAGAATTGCTGGGCTATCGACGGTCCAGCACAGGAAAAGGTCTATGCCGCGACCGGGTGGACC
GCTATGCGCGGCCAACGGCTGGATGACAGCATCGATGACTCCAAGAAACGCGACCACTACGCCATTCAAGCGGTGCTC
GGTTCCCGACCGCACATGATGCCGAAGAATTCTACAGCTCCTCCG (SEQ ID NO. 224)

Clone Rv223

::::::::::Rv223IS1081N1400.seq::::::::::
CGCGACTGGCTCCCCGGNCGGCTGCTCGGGTCCGCCGATAGAGACCGGGATGTGCCCCGACGACGGGCAGCCGGGTTG
CGTGGGACGGGGCGGGGGTTCGGGCAGCCCAAGCAACGGGCTAGTCCCCGAATCCTACGGAGCCGTACCTACGCCTAC
GTAATAGTAGCTATCAATAACAGTTGACATACGCCAACGATCTGTGAGATCAATATTGCCTGACGCATGTCAAGACAGG
CGTCAAGACAGGTGTCAATAATTGCTCCGCTGGTGACGGTAACCGGTCGTGCGGGTGTGTGACGCCAAGGAAGGAG
TGTGGGTGGTGACGCTGAGAGTGGTTCTGAGGGTTTGGCGGCCGCCAGTGCGGCGGTGGAGGCGTTGACCGCACGGC
TGGCCCGCCGACACGCTGGCGCGGCGCGGCGATTACGGCGGTGGTGGCGCCCGCGGCGGATCCGGTGTGTTGCAGA
ATGCGGTGGGGTTTAGCGCTTAAGTAGCCAGCATGCCGCGATCGCCGGCGAAAGGGTCCAAGAACTGGGT

(SEQ ID NO. 225)

::::::::::Rv223SP6.seq::::::::::
ATACTCAAGCTTATTGAACCGCGGTCGCGAGGCAAGTGGACCTCATAACGACTCGGGTCCAGCGACCGCGCCAACAC
GAACGGCCGGACGACGTTGGGCCAGGGTCGCGGCTCCCTACAAACAGGATCCGTTGCCGCGAAGACAGGCTCCGG
TGCGGCGTTGGGCGCGTCTGCTCCAGCGTCCGGTCCCGGTCGCGGCGACGCTTGTTCCTCCATCTCGCCCC
CTAATCTCGAGGACGCCGTACCCGCGAGGCAACCTCCAAAAATGCAATCCCGCAAAATGCAATGCGTCNAGCTATTT
CTCACACCGACCGTAGTTGCGGATCAGAAATCCGTTGGGCGCGGAAGTCCAGCCGAATTTGTTCTCCGCTCCGCAT
CATGCTTGTAATCGTTTGAAATTCATCCTCATATGCCTCGATCGCTTCATAGGGTCCAGGCCCAAACCCGGGCAGGA
CTGGGTGGCCGTTGATGTTGGAATCCTCCACTACTAGGTATTCACCGGC (SEQ ID NO. 226)

::::::::::Rv223T7.seq::::::::::
GTCTCGATCATGGCCAAAGAGCTCGACGAAGCCGTAGAGGCGTTTCGGACCCGCCGCTCGATGCCGGCCCGTATACC
TTCCTCGCCGCGACGCCCTGGTGTCAAGGTGCGCGAGGACGGCCGCTCGTGGGGTGCACACCTTGATCGCCACC
GGCGTCAACGCCGAGGGCTACCGAGAGATCCTGGGCATCCAGGTCACTCCGCCGAGGACGGGGCCGGTGGCTGGCG
TTCTTCCGCGACCTGGTCGCCCGCGGCTGTCCGGGTGCGGCTGGTACCGGCGACGCCACGCCGCGCTGGTGGCC
CGATCGCGCGCCACCTGCCGCGAGCGGCTGCGAGCGCTGCAAGCCACTACGCGAGCCAATCTGATGGCAGCCACC
CCGAAGCCCTCTGGCCGTGGGTGCGCACCCTGCTGCACTCCATCTACGACCGCCGACGCCGAATCAGTTGTTGCC
AATATGATCGGGTCTCGAC (SEQ ID NO. 227)

Clone Rv224

::::::::::Rv224SP6.seq::::::::::
ATACTCAAGCTTTCGTGAGTTGATGCGCCAGCAGACCAACAAGAGCATCGGGACATACGGAGTCAACTACCGGCCA
ACGGTGATTTCTGGCCGCGCTGACGGCGCGAAGCAGCCAGCGACCATTCAGCAAAATGGCCAGCGCGTGCCGGG

CCACGAGGTTGGTGCTCGGCGGCTACTCCCAGGTTGCGGCCGTGATCAAGATCTTCACCGCCGACCACTGCCCGGCC
TCGGGTTACGCATCCGTTTGGCCGCCGCC (SEQ ID NO. 228)

.....Rv224T7.seq:.....
GCCCCGTGTAATTTGGGATGGGCAAAAAGCGAAGCACCGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGGCT
AGGGCTTCTCGCGGAAGGCCCGAACGTACGGCGTTTCAACACGTGCGCTCGCCCTCCGACCGGAACATTCTGGGGAT
GGCAGCAACCTGGTAGCACCTGGCCGGGCGATGATCTGCAGCGTCGCCGCGGGTAGTCTCCGCCCCGGCCGC
(SEQ ID NO. 229)

Clone Rv225

.....Rv225SP6.seq:.....
ATACTCAAGCTTCTTTGACCGAACGCGTCCACCGCACCGTGAGATTGGTGGCGCCATTCTGTCGTGGTGTAGCTGCTG
TTGGCGCGGTGAGGCGTTTCGGCGAGGAGGTAGTGTCTACCCCAAGTTCGGCACTTCCGCAACCG
CCCAGCTCGACCGCAATTACGGCGGCCGCAACGGCCGCCGGAAGGCGTCACGCAATCGCTTATCCTTCCAGGTTCC
CAATCTCCGCTTACTTGGGTCTTCATCGG (SEQ ID NO. 230)

.....Rv225T7.seq:.....
GGCAGCGGCGACAACCGGAACGTCCGCACGGTGCTCAATCACGGGTGCACGGTGTGCATCAGAATGGCGGGGTTTCGT
TGTGCGCGGTGAGGCGTTTCGGCGAGGAGGTAGTGTCTACCCCTTGCCCGCGGGTTCGTGCGGACTGAAAGGGATTTCAT
TGGGAACCCACGGCTGCGTATCGCAGGGCCTCGGTGACGTCTGCTTCCTCNAGCTCAGGAAGTTCGGCGAGAATCTCG
GTGGATGTTATTTGGTCCGCCTAC (SEQ ID NO. 231)

Clone Rv226

.....Rv226SP6.seq:.....
ATACTCAAGCTTCTCGGCTTCTCTGATAGCCTGAGAAGAAACCCCAAGTTAATCCGCTGCTTCACCTATTCTCCAGC
GCCGGGTATTTTCTCGCTTCCGGGCTGTCATCATTAACTGTGCAATGGCGATAGCCTTCGTCAATTCATGACCAG
CGTTTATGCACTGGTTAAGTGTTTCCATGAGTTTCATTCTGAACATCCTTTATTATTGTTTTCGCTT
(SEQ ID NO. 232)

Clone Rv227

.....Rv227SP6.seq:.....
ATACTCAAGCTTGGTGACCGGCACCGGATACGTTGCGGCAGGCATCTGGGCTGGCGGTGGTTCCGCGCTCCGAAGCC
GTCGAACACCATCGCCAGCGCGGCTTCCACATCAACGACCATTTCCGGCCAGCTTGGCGCGCATCAGCGGCTTGTGAT
GAGCGCCCCACCGAATGCCCGCGCTGCCCGGCGTATCACATCGATTTCGACCATCGCGCGGCGCGGTTGCCGAGGGC
GAACGAGGCGGTGCCAACCGCAATCTGTTTGGTCAGTCCCTCATGCGGGTTGATTCTTGCCGTCCGGACGGGGCC
GCGTCATGCGCTCGGTTCCGC (SEQ ID NO. 233)

.....Rv227T7.seq:.....
CCGTTGCGCAGCGTGAGCCGATAGTTGACATCCGGCTCGGTGAAGGTGAAATCGATGGCCAGGTCGAGGTCCCATGCG
CGTGGGCCATTGATGCTGATCGCCAGGACGTCAAAGATTTGGTCCGGCGTCAGCTGGGCGAAAAACGTGGGCGCCGGG
ACTTGCCCGGAGCTGCCCGGTTCCCGTCCGCGAGCTCGGCGGCCCCGGTCAGAAAGAAATTGCGCCAGGTCGCACAC
TCCGCGCCGTAGGCCAGCTGCTCCAGGGTGTCCGCATAGAGCCCGGGCCGACGCGTGTCTGCTGTCGGCGAACACC
GCATGGTCGAGAAGCGTTGCCGCCAACGGGAATCACCTGCGTTCGAAAGCTTCGCGGGCCAGCTCCAGCACTCGGT
GATGCCACCAACGCGT (SEQ ID NO. 234)

Clone Rv228

.....Rv228SP6.seq:.....
ATACTCAAGCTTGGCGATGTTACCCCTGACAGCGTGAACATATGTCNAAACACACGGCACCGGAACGGTGTGGGGGAC
CCCATCGAGTTTCGAGTCGCTGGCGGCCACTTATGGCCTGGGTAAAGGCCAGGGCGAGAGCCCGTGCATTTGGGGTCTG
GTCAAAACCAACATCGGCCACCTGGAGGCGGCGCCGGTGTGGCTGGATTTCATCAAGGCGGTGCTGGCGGTGCAACGT
GGGCACATTTCCCGCAACTTGCACTTACCCCGTGGAACCCGGCCATCAACACGTGCGGACGCGGCTGTTTGGTGGCG
ACCGAAAGCGCCCCGTGGCCGGCGGCTGCCGGTCCACGAGGGTGCAGTTCATCGTTCCGCTCAGCGGGACCAA
(SEQ ID NO. 235)

.....Rv228T7.seq:.....
CCGGTAACAGATCAGCTCGTACCTCACTGCCGGGGTGAATTCCCCACCGGTGCTGCGCGCTGCCAGTAGTGCA
CCTTCTTGACGCCTCGAAAAGGGGAGTCGGTGGGTAGGTACCGTCAGGAGCCGCCTACCCAGGTTGGCGCGGTGAC
CGGTCTCTCGAGTATCTCCGCAACCGCCCCACCGGTGCGGTCTCGCCCGGATCCACTTTGCCCTTGGGCAGCGACC
AGTCGTGTAACGGGGCGGTGAATGACAGCGATCTCGACCGGCCCTTCCGAATCGGCACTGCCGGGTGCGCAGAACA
CCGACCGGCGGCGTACACAATCCGGCCCGGAGCGCCGGCGGGCGGACGANTTCTGGATCGACACCTCAACTCCTG
CAGGTCAATTCGGCCAAGCTGCTCGCGGTGCTGGATGTGGT (SEQ ID NO. 236)

Clone Rv229

.....Rv229SP6.seq.....
ATACTCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCACCCACACGCGCGGGTCGGGCGCCGGGCCCGG
GCCGCCAGGCTGCTCCGCTCGGTGATGGCAGCCACCGCGACACCACCCGGCTGCGCTACGTCGAGCCATACCGGGCG
GAGCTACATCGGCTCGGCCGCCAGTGTTCCGGGCCCTCTTTCGAGGTCGAGGTTATACCGATTGCGCATCCGCAGC
CGCACCTGGTCTGCTACCGTGCCCTACCTCTGCTGTCGGGCGGGCCA (SEQ ID NO. 237)

.....Rv229T7.seq.....
TCCGTACGGCCCGGGTACGCTTCGGTCGCAGTGTGCGAGTGATAGATGACGACCGGGACCTCGTCGGCATCTTCCATA
GCCCCCACACCTTCAGTTGCTCACCAGGAATCCAACCGGTAGAAGGTCGGCGAGCGCTCGGCATTGGTCATCGGGATA
TGCCGCTCGGGACGGTCAGAGCCCTCGGTCCGGCCAGCACTCCGCAGGCTTCGTCGGGGTGGTCGCGACGCGCATGG
GCCACCATCCATCCACAGGTCTGCGCAATCACCCGC (SEQ ID NO. 238)

Clone Rv22

.....Rv22SP6.seq.....
GGACACATTGCGAACATTGATGACAAAATAGAAATCATTGATGGTTTGAGTCACCAGGCCGATCAAGCCTTCGCCGAG
CCAAATTCCAATCAAGAGGCCCAAGCCCGTACCAATCAGCCCGGCAACGAGGGATTCCGTATTATCAGCCAAAATAA
CTGCTCTCGGGTTACACCCAAACAGCGCAATATGGCGAAAAACGGTCGCCGTTGCACGACATTAAATGTCACGGTATT
GTAAATTAAAAAGATAACCCACCAACAAGGCAATCAAACCTGAGAGCGGTTAAATTGACCGTAAAGCGTCCGTATCTG
TTTGACGGTGTCCCGTTGGGTNTCCGACGTTTCCATACGCACACCGGCCCGGCGAGTCTTTGTTGGATGCGTGTTCAGT
GGCTCATCTTTGATGATCA (SEQ ID NO. 239)

.....Rv22T7.seq.....
GCCTGGCCAGGTGAAGGCCGACCTCGACGCCAAAGCCGCTGATCCGGCACATGAGTCGGTGGACTGGGACTTGAAGT
CGCTGCGATGGGCGTGGAACCGAGCCAAAGATGACGTGGCGCCGTGGTGGGCCGAGAATCCAAGGAGTGCTACTCGT
CGGGGTTGGCCGATCTGGCCAGGGCCTGGCTAATTGGAAAGCTGGCAAGAACGGGACCCGCAAAGGCCGGCGGGTGG
GCTTCCCGCGATTCAAATCCGGGCGGCGTGATCCTGGCAGGGTGCCGTTTACCACCGGCACCATGCGCATAGAGGATG
ACCGGCGCACGATCACGGTCCCGGTGATCGGGCCGCTGCGGGCCAAGGAGAACACCCCGGGTGCAACGCCACCTCG
TGAGCGGGCGCGCGCAGATCCTGAACATGACCTTGTGCGAGCGGTGGGG (SEQ ID NO. 240)

Clone Rv230

.....Rv230SP6.seq.....
TAACCTCAAGCTTCAAGTCCGCGNGTCCGACCCTGTTTCGACGGCTACCTGAATCAACCCGATGCCCGCCGCGCGCTTCG
ACCCGACAGCTGGTACCGCACCGGCGACGTGCGCGGTGGTCGACGGCAGTGGGATGCACCGCATCGTGGGACGCGAGTC
GGTCGACTTGATCAAGTCGGGTGGATACCGGGTCCGGCGCCGGTGAAATTGAAACGGTGCTGCTCGGGCATCCGGACGT
GGCGGANGCGGCAGTCGTGCGGGTGCTCGACTATTATCTAGGCCAGCGGATCGTTGCCTACGTAGTCGGCTCAGCGAA
TGTCGATGCGGACGGGCTTATCAACTTTGTTGCCCAACAACCTT (SEQ ID NO. 241)

.....Rv230T7.seq.....
CCATGTCGCCCAACATATCGTCGATGTTTCGCGTCGTCCGCCCTCGCGCACGTGGTCTGTCACCAGTCAACGTTAACGCC
GCCGCACATGTCCTGCGGCCGGGCAAAACGTGAAAACGAGCGGGCGACTGCAATGTCATGACACCGACGCCGCCGA
TGGGCCAGGGTCTGGCAGATTGATCTGTGCGGCCAGTGCCAGCAGCGTCGCTCGTATACGGCCGGCCGACGAGT
TGAACCGACATGGGCATGCCGTGCGCGTCGAAGTCCACGGCACACGGCCGCGGGTGGCCGGTCAGATTCCANACT
TGAAAGTACTGAAGCCGCTGCACCACGAG (SEQ ID NO. 242)

Clone Rv231

.....Rv231SP6.seq.....
CGAAAGCGTGAAACAGCTCGCGGCAGCCCCGACGTGCTGCGTCCGATAGCCGGCGGGCGAAGATCAATTCCAGGCAG
CTCCCGGACAATGCGGCTCTGCTGGCCCGCAACGAAGACTCGAGGTCAACCCGGTGCCCGGGGTGCTGGTGACCTG
CCGATCGCACAGGTTGGCCACAACCGGCCGCTTGATGCCCGGTCCGCAAGCCCGGAGTTGCCAAACCCAGCGTGAT
CNTGCTCNGCTCTNTANTTCGGCGAAGAAGTGGCTCGCCTGATCACCTACCATCGGCCAGGATCTGCGTGTATCACA
ACGCTCGCCAAGGAGGTTGTTGTG (SEQ ID NO. 243)

.....Rv231T7.seq.....
TCCGCCACGCTTCGCGCCGCGCCGATACGGCGCGTACCGATCTCCGCGTCATACACCGCGGGTAATCGCCGACGGTG
CCGGTTCGCGAGCCGAAGGTGACGACGCTGATTGAATCGAGTTCCAGGTCCAGCGGGTGGCGCAGCAACGGCGGAGC
TCAACGACGTCAATCAGTTGTCGTTTCTACGGTCACCGACCCGGTGACCGTAGTCGCCCCGGTGCCTCGGCCGAGA
AGCTGCACCGCCACCGCGACACCGTCTTGACGCGGACCCACCCCGGATCGGTTGTTGGCCAAGGTAATTGGGTC
ATTCCATTGACGGGACGCCGACCC (SEQ ID NO. 244)

Clone Rv232

:::Rv232SP6.seq:::

CATTCTTTAACAGTTGTTTTGGGCTCGGCATGGTTAGCCAACGTTCTGCGGTCCACCATATCATCTTGGTCCGGTAGC
GCTCGTCCGGGGTATGCTGCCGCCGGGATTCTCGCTGCTATTACTCCCCCGAAGAACC GCCACC GTCCAGCGCGTG
GGCCGNCGCGGTCCCATCACAACTGAACCCCAACAGGGACATGCTTATCGGTAGGGCGCGGCCAAGGCGGCAGCA
ATCGCATCACTGCGCTCTGCGCGTCACTATTAAACCCACCCGGACTTCAC'TCCACCACCCCGAATGGCGCCCGGT CAT
TGATCATCTGGCGCACCGCGGATAA (SEQ ID NO. 245)

:::Rv232T7.seq:::

CGGTGTCTGCAGTTGGTAGGCCTGCAGTTTGTGCATCATGCCGATGCCCGGCCCTCGTGGCCACGCATGTACAGCAC
CACGCCGCGCCCTCACGGGCGAACATCGCCAGCGCGGCGTCCAGCTGAAGCCCGCAATCGCAGCGGCGTGACCAAAC
ACATCGCCGGTCAAGCACTCCGAATGCACCGGACCAGCACGTCGTACCCGTGCGCGTTGGGCGCGGCGATCTCGCCGC
GGACCATGCGCGACATGTTCCACGTCTCTANATGCTGGTGTAGCCGATGGCGCGAACTCCCATGACGAGTCGGA
ATCCGCGCCTCGGCGACCCGCTCAATGTGCT (SEQ ID NO. 246)

Clone Rv233

:::Rv233SP6.seq:::

CGGCATCTGGCGGTGAACCTGTTCTTGGGCAACATGCCGAGGATCGCCTCTTCCACCACGCGGTGGGGTGGCGTTG
CATTACCTCACCGATGGTGCGCTTGTGCAGGCCCGGATACCCGAGTGCCGGTAAACCATCTTGTGCTGCAGTTT
GTCGCCGCTGATGGCGACCTTGTGCGCGTTGATCAGCATNACNAATCACCGCCANCGACATTGGGGGCGAACGTCGGC
TCGTGCTTGCCGCGCAGCAGGCTGGCCGCCGCGACGCAAGGCGCCAACCACACGTCCGTGGCGTCGATGACGTACCA
CCATCGCGTGGTGTACCCGCTTGGGC (SEQ ID NO. 247)

:::Rv233T7.seq:::

GCGGCAAAATTGAAGCACTCNTGGCCACTNCCGCCGGAGGGACAATCTCGGGCGGCTAGGGCTTCTCGCGGGAAGG
CCCGAACGTACTGCGTTTCAACACGTGCGCTCGCCCTCCGACCGCAACATTCTGGGATGGCAGCAACCTGTAGCAC
CCTGGCCGGGCGATGATCTGCAGCGTCGCCGCGGGTAGTCGCCCCGGGCGGCTACAGTCTGAAACGCGATGACCATC
GATGTGTGGACGCCGCATCCGACNCAACGGTTCTTACACTGTGATATGTTGCGCTCGCTGCGCCGGTGGACGGTGGGT
CTATCCCGGA (SEQ ID NO. 248)

Clone Rv234

:::Rv234SP6.seq:::

CGCGTTGAAGTGAAGGGGTGCCGCCCGGCTCGAGCAGGCAAGCCATTTGTTGATGCGGTTACCGAAGATCTTTTCGG
TGACTGCCCGCCGCCGCGCAGCTCGGCTCAGTGTCCGGCGTTGGTTCGCCGCGGCGACAATCTTGGCGTCCACGGTGGT
CGGGGTGATGCCCGCGAGCAGGATTGGCGAGCGGNCGGTCAGCCGGGTGAACTTCGTCAAGAGCTGACGCTGCGGTTG
GGGAGGCGAATCATGGTCGGTGCGTAGCCTCGACTAGGCCCGGG (SEQ ID NO. 249)

:::Rv234T7.seq:::

TGACAACGCGGCGCGGATTACCCCGCTACCGCAGCAGCATGACGCGGTAGCGAACACCGCCGGATGCAGCGCAGGTGC
GTCGATGTGCTCACGGAATCGCCCCGGCACCGCATCTCGAGGATCACCAAGTCCACCCCTGCAGCGCGACACCGAC
GATTCGCTACACCGCCACGCCGATCAGGCCCTGGGCCAGCTGATTGGAGCTGGCGTATATGGCGGCGATGGTGACGAT
GGTCATCGCCTTTACATTGTGGCGGCCAGAACACGGCGTTGGGGCGGCGGTGATGAACACTAGGCGACCANATCC
CCGGGTCAACAGGTTGACCATCC (SEQ ID NO. 250)

Clone Rv235

:::Rv235SP6.seq:::

CGCGGACATCCCGAACGAGGACACGCGACCGCTTCGGTGTGTGATCTATCAGGGCTCGCACACGCGCAACCGCTTCC
GGCTACCTAGACGCGGT (SEQ ID NO. 251)

:::Rv235T7.seq:::

GCATGCGGGTGATGCCGTTCTCAGTGCGCAACAGCGTTGACGCGGCATACCCAGCCGCACATGCCGTGCACGCCGNG
GCCGGGGCGGGAATCT (SEQ ID NO. 252)

Clone Rv237

:::Rv237SP6.seq:::

CTCAAGCTTCAGNCCNTCTAAGCGGTCTGCGCGGCGATCGCAAAGATCGCCCTTTGCCGGCGTTGGGGGCTTCTGCTC
GGGGGTGTTGTACACCTTCTCGAACACCTCGGCACCGACACCACCGCTCGGCTTGAACACCGCCAACATCGGCAGC

ANATCTTGATGTCCTGGTGAATCCACGGTGACTTTGGAGTGGAAGGCGGCCATACTGATCGCGCGGCCACCATGA
GCTAGCGGCAGGAAAACAGCAGCCGCTCACCTTGCGCAGCAGCGTCGGGTGATATGCCTGGCGCCC

.....Rv237T7.seq:.....

(SEQ ID NO. 253)

AGTCGAANGTCAGTCCGGTCTCCTCTCCGACTACGGCCAAGAACTGGGGCGACGGGTGTGAGTCAGAACAGCGGAAAC
TGGTGGCGCCTAGGCGAGCGAACGCTCACAAACGGCGGTGACCGCTTCTGGTCTGACCATCGAGCCGTGCCAGC
CCGGCCGCGTGCCGTGAGCCGCATCCACTGGATGCCCTTCTCGGCGGTTTCAATCANGTACAGGCGACGTTCCGCCACC
ATCGTGCCGGGGCAGGTTAGCGAGAAACGCCGACTTCACCGATTGCCCTCGGTGATGxxxxx (SEQ ID NO. 254)

Clone Rv23

.....Rv23T7.seq:.....

AGCTTCGCGGCGTGGCGATCGCGGTTCAAGGCGCGCTCTTCGAGCACAACGAGCGAAGACAGCTCGGGCGACGGAGCCT
TTATCGACATCCGTTTGGGCTGGCTGACCGGCGGCGAAGAACTGCTGGACGCGTTGTTGTCGACGGTGCCGTGGCGAG
CCGAGCGCGTCAGATGTNCGACCGGGTGGTTCGATGTGCCGCGGCTGGTGAGTTTTCACGACCTGACCATCGAAGATC
CGCCGATCCGACGCTGGCGCGGATGCGCCGCGGCTCAACGACATCTACGGCGGCGAACTGGGTGAGCCCTTACCA
CCGCGGGGCTGTGCTACTACCGCGACGGCTCTGACAGCGTCGCCCTGGCATGGCGACACCATTGGTTCGCGGCAGCACTG
AGGACACTATGGTGGCGATCGTCAGCCTCGGCGCCACCCGCGTCTTCGCGCTGCGGCCGCGTGG (SEQ ID NO. 255)

Clone Rv240

.....Rv240SP6.seq:.....

AGCTTCAGCTGATACTCGACCAGCCCCACTCGGGCCAATACGTGAATGTCTAGCATCTTCACCCGTTACGGGGCTANT
CGAGTAGTAGACATTGATTAGCCTGAACGTACCTCCGACGCCAGCTGACGAACGGGTATGACGGATGGATTTCTGGGT
GTCGCGCCCGAGGTCAATTCTTACGGATGTATCTCGGGGCCGATCGGGGCCGATGTTGGCGGCCGCGGCGGCTGG
GACGGACTATCCGACGAACGGCGGTGGCGGCGTCTGGTTTGGGTGCGTGACCTCGGGCCTGGCGGATGCGGCGTGG
CGCGGCCCGCGGCGGTTGCGATGGCNCGCGCGGT (SEQ ID NO. 256)

.....Rv240T7.seq:.....

CTGGTCATGGACGTTGCTCCGGTAGTGGCTCACTGCCGATCCTCCTCGTTGAGAGTGCCACCTCAGGGTTGGGTAGGG
TTGGGTACTCGAAACCAAGTTACCCACCAAGTAACACCGTCAAATATATCCGTTGCATAGGTCAATGCAAGTTGATGT
GAGCTACATTGCACCAACTAACTAACCAACCGGTTGGGTAGCGGTGATCCTGGCCGTGTCGGTCTCTACCTGCGG
TGATAGCGATCAAATGAAGAATATGCGGAGTCTAGGGCGGCAGCGCCTGGCANCCTAGATCATCGGCTCACGCGGATG
CGGCCTCTTGGTACGGACATGCGCGCG (SEQ ID NO. 257)

Clone Rv241

.....Rv241SP6.seq:.....

CTCGTAGTAGCACCCCTGTAATTTGGGATCGGCAAAAAGGCGAATCACCGCGTGGCCACGACACGCCGGGAGGGACN
ATCTCGGGCGGCTAGGGCTTCTCGCGGGAAGGCCCGAACGTACGGCGTTTCAACACGTGCGCTCGCCCTCCGACCGCG
AACATTCGGGGATGGCAGCAACCTGG (SEQ ID NO. 258)

.....Rv241T7.seq:.....

GGATCAACTACCGGCCAACGGTGATTCTTGGGCGCGCTGACGCGCGAACGACCCAGCGACACATTGAGCAGATGGCC
AGCGCGTGCCGGGCCACGATGTTGGTGCTCGGCGGCTACTCCCATGGTGGCGCNCGTGATGACATCGTCACCGCCCGC
ACCACTGCCGGCCTCGGGTTCACGCAGCCGTTGCCGCCCGCAGCGGACGATCACATC (SEQ ID NO. 259)

Clone Rv243

.....Rv243SP6.seq:.....

AGGACCGTCAGCACGGCGACGTGCTACTCGCCGAGCAGTGGGAATCGCTCTGCAGCAAACCATTAATCTGCGCGACGT
TCGAGATGACCTTCTGAATGGACGGATCTACCTGCCGCGCAGCAGCTGGACCGCGTATGCGTCCGCCCTCCGCCTGGA
CGACACCGGGGCACTCTATGACCCCGACGGACGGCTCGCGGTACTGCTGCGGTTACCCGCCGACGCCCGCACGGTACG
CGTCGGGACTGCGCTGAGTCCANCCTCGACGCCGTAGCGCTGCTGCTGTCGGGCCATGTCTGGCATCTACCGCCGTCG
CTCCCTTGA (SEQ ID NO. 260)

.....Rv243T7.seq:.....

CGACTCTGTTGGCCACTGCGGGTCGATCTTGCGGCCGCCCGGTCGTGGAAACGCCCAGGTACCCCGCGGGCGCACCGC
GGTCAGCGCGTCGTTGGCCAGCGTGGTCACATGGAAAGTGGTCGACGACGAGCTTGGCGTTGGGCAGCAGCCCGGGCGT
GCGGATCGCCGAGGCGTATGACGCGCGGGGTGATGCGCCACCGTACTGGATGCTCTCCCGGAAGTGGGTGTGCGCG
CTTGACAGCATGCCAGCACCGCGCGCGCGCGGCGCTTCATGCTGCCCATAAACCTGATACCGGCCAGGTTCGACNA
ACNGTATCCACGGTCAACCC (SEQ ID NO. 261)

Clone Rv244

.....:Rv244SP6.seq:.....:
CACACGGACGGCGGTGCGGACGCAGCTGACGCGCATGGTGGTCAGCATCGCGGCCGGTCTGCTGTTGTATGCCTACTT
CGCGCCGCGCAAATGCTGGTGGGCGGCGGTGGTGGCGCTCGCATGGCTGGGCTGGGTGCTGACCCAACTCTCGAACCA
CACCGGTGGGTGGGCTGGGCTATGGCCTGCCATATCGGCCTGGTGTCTACN (SEQ ID NO. 262)

.....:Rv244T7.seq:.....:
CCGATATCCGAGCCGATAGCTGGCGGGCTCGGTGGTNGCCAGCGGCGCTGCGACGAAAGTGTGACCGTCATGAAACA
GACACCACGGCGGCCGTGCGCCGTGCTCACCTGCTCGAGATCTCAGCATCCGCGAGCCGGTGTGATCGCGCTTTTCGGC
GTGTAGTGGGTGCGCGCCCGAGCCCGGCAAACGCCGCGCCGACACAACCCCGGAACAGGAAGTCCGGTCACCGCGCC
(SEQ ID NO. 263)

Clone Rv245

.....:Rv245SP6.seq:.....:
GCTTCAGGACAAATTGNATCCCTATGCACCCGTTGTCACGCCGATGAGTGAAGACTGCACGCAATCGCCGGAATCCGG
CAAAACCCTGCACAAGCGAAATCAACCGGAGGCTGACAAGGCAACGTCGGTGATCCGTACCGCCTGGTTGGACAAACG
GCAGAAGGCGCCTCGTCCGGTCCATCTACGCCGAGCACACTGGTGATAGCGCCATCGGCATCGGTGCGGCCACGGTGG
AGACGAACGTCCGCNGGCGTCTGGGTGAGTAACCCGCCGACAGTTCTCGGGCAAGCTGGTCAACATCGGCGCCACG
TCTCCAAC (SEQ ID NO. 264)

.....:Rv245T7.seq:.....:
GTTTGGCGCCTTATTGCACTGAGGTGCTCAATTGACCCACAGCGGAAATGCCGACTATTGCGAGGCCTCCTTCGCCT
TGGCTGCCGGAGATGGGCTCCGCGGGAACCGCATGCAGGTATATGACCTCGGTTTCTCGGGTGCTACCGCGTGCCTTG
TCGAGGATGAACTCGGCGTTGGAATTGTCCAGCCGGCCCAATTCATCGAGCGCAGATTTCGTACACATGGCCGGCGGCG
ACATACCTTACCCTGGATCTGCTCCACACGGACCGCCCTGTGCGGATCTGCTCACGGGTAAAGGAATTA
(SEQ ID NO. 265)

Clone Rv246

.....:Rv246SP6.seq:.....:
GCGCACTCCTCCTTATCGCTCCGCTCTGCATCGTCGCGGCGCGGTGTCAGGTGCAAACGCCTTCGGGGGTGGGGGTCTTG
CGGAGCACACCGGATACGGAGCGCAACGCGTCGCGTTGTGCGGGCAAACAAGTGTGCAGGNCCATGCCATGTCCAG
CAGCTTATCAGTGTGCAACGTGCGAACGTGCGCCTTCGCCGGTGCTGAATCTCTACAAG (SEQ ID NO. 266)

.....:Rv246T7.seq:.....:
CGCTGAAAGCCACCATTCGCGGGTCGGGCGCCGGGCTCGGGCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCG
CGACACCACCGGCTGCGCTACGTGAGCCATACCGGGCGGAGCTACATCGGCTCGGCCGCCTAGTGTTCGGGNCCTC
TTTCGAGGTGAGGTGCA (SEQ ID NO. 267)

Clone Rv247

.....:Rv247SP6.seq:.....:
TGTAATTTGGGATGGGCAAAAAGCAAANCACCGCTGGCCACAAACGCGGGGAGGGACAATCTCGGGCGGCTAGGGCT
TCTCGCGGGAAGCCGAAACGTACGGCGTTTCAACACGTGCGCTCGCTCCGACGCGAAATTCGGG (SEQ ID NO. 268)

.....:Rv247T7.seq:.....:
CTTGGGCAACATGCTGAGGATCGCCTTTTCACCACGCGGTGCGGGTGCGTTGCATTAGCTACCGATGGTGCGCTTG
TTGCAGGCCGCGGGGATACCCGAGTGCCGGTAAACCATCTTGTGCTGCAGTTTGTCCGCTGATGGCGACCTTGTGCG
GTTGATCACGATGACGAAGTCACCGCCATCGACATTGGGGGCGAACTCGGCTTGTGCTTG (SEQ ID NO. 269)

Clone Rv249

.....:Rv249SP6.seq:.....:
GCATGCTTCATTATCTAATCTCCAGCCGTGGTTAATCAGACGATCGAAAATTTCATGCAGACGGTCCCAAATAGAAAG
ACATTCTCCAGGCACCAAGTTGAAGAGGTTGATCAATGGTCTGTTCAAAAACAAGTTCTCATCCGATTGAACTTTACC
AACTTCATCCGTTTCATGTACAACATTTTGTAGAANCATGCTTC (SEQ ID NO. 270)

Clone Rv24

.....:Rv24SP6.seq:.....:
ATACTCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCAGCCACCACGCGCGGGTGGGGCGCCGGGCCCGG
GCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACCACCGGCTGCGCTACGTCTATCCATACCGGGCG
GAGCTACATCGGCTCGGCCGCCCATTTGTTGNGCCCTCTTTTCAGGTGAGGTCTATACCGATTGCGCATCCG
(SEQ ID NO. 271)

.....Rv24T7.seq:.....
TCCGTACTGGTCGGGTACGCTTCGGTCGCAGTGTGCGAGTGATAGATGACGACCGGGACCTCGTCGGCATCTTCCATA
GCCCCCACACCTTCAGTTGCTCACCAGGAATCCAACCGGTAGAAGTTCGGCGAGCGCTCGGCATTGGTCATCGGGATA
TGCCGCTCGGGACGGTCAGAACCTCGGGTCCG (SEQ ID NO. 272)

Clone Rv251

.....Rv251SP6.seq:.....
GTTCTCGCACGATTTTCGGATTAGCGGGATGGTCTCAATTGGGTATGCGGGGAAGGCGCTGACATTCGCCGCGATTAGC
TGTTTGATGGACCGGGGGTATTTTGTATCACGAAATGGGTGTTTATNCAGGTCGCACGCTTTCATCCGGGGCGGAA
CG (SEQ ID NO. 273)

.....Rv251T7.seq:.....
GGGTGTGCCTGCTGTGTATGCACGGCATAACGACATCCTTCCCCTGAAGACCGCGGTGGAACAGCCACGTGTCCATC
ATCANGGGGTCAACCCCGGCCAAGGGCGACGGCACGCCAAGTTCGCCGACCGTTAACCTAGTGCTGTAGCTTCATT
GCTGCGAGCAAAACAGCTGGTCGGNCGTTAGGAATGAATTGAACTCAACCGATTGGTGCCGCCGTAGGTGTCCTGG
CTG (SEQ ID NO. 274)

Clone Rv252

.....Rv252T7.seq:.....
ACTACCGGCCAACGGTGATNTCTTGGCCGCCGCTGACNGCGCGAACGACGCCAGCGACCACATTCAGCAGATGGCCA
GCGCGTGCCGGGCCACGANGTTGGTGCTCGGCGGCTACTCCCANGGTGCGGNCGTGATCGACATCNTCACCGCCGCAC
CACTGCCCGGCCCTCGGGTTACACGCCGTTGCCGCCCGCAGCGGACGATCACATCGCTTTTATTNNTNTTCNGGAAT
CCCTCGGGCCCGCTGGCGGGCTGATGA (SEQ ID NO. 275)

Clone Rv253

.....Rv253SP6.seq:.....
ACGTCGGGANACTGTTTCGCGTTCATCCTCGTCTCGGCGGATTGGTCTGCTGCGCCGGACCGACCGATCTTCAGCGGGG
GGTCACGCTCCGTGGGGTGCCGTTACTTCCGATCGCCAGTGTGCGCGTGCTGTGGCTGATGCTGAACCTCACCGCGT
TGANTTGGATCGGTTCCGGATCTGGCTGGTGGCCGGAACGCNATTTATGTCGCTACGGGCGCCGGC (SEQ ID NO. 276)

.....Rv253T7.seq:.....
GCTCAAAGGCACTACTGGCACCAAGGCCACACGTACCTGTGACTCCTGCGCCGACCCGCCGAGGTCTGGCCGTTA
CACCGAACGGGCGAGCCGGGAGTTGGTACCATCGAACAAGACAAGGTGCATGGGCGGAGTTGTTCCGCCACTTCGTCG
ATGACGGGTC (SEQ ID NO. 277)

Clone Rv254

.....Rv254SP6.seq:.....
CGATACCGGCTGCTTACCGAGACATCCACCATGCCACCCGAATCACCGCACGCGCCGAAATCGCACAAACAGCTTGACG
CCTTGACAGGTTCCGCGATTGGAATTGCCGACGGTCTCTGACGGCGTCGACCTTGGCAGCCTCTACGAGCTCTCGGAAT
CACTTGCCCAGCAGGGGTTTCGATGAGTGTACACCGAAGACCTCGATATGGGCGCAATCCTGGCCGACACATCCAAC
CGGGTGTTGTGTGCTGCGGCGCCGGTGGGGTCNGCAANACACTACCGCGGCGCGGCTGGCGTTGCGCGCGGCCGAAT
ATGGCCGCACTGTGGTCG (SEQ ID NO. 278)

.....Rv254T7.seq:.....
CGTCGTCGTCGTGGTATGCGATAGCCATCCCGTCGGGCTACTCGCCATCACCGATCAGCTTCGCCCCGAAGCCGCCGC
GGCGATTTCCGCTGCGACCAAACCTGACCGGGGCCAAACCGGTATTGCTTACCGGCGACAACCGGGCCACCGCCGATCG
GCTCGGTGTACANGTTGGCATCGACGACGTACGGGCCGGGCTACTGCCGACGACAANGTCGACGCCGTGCGNGCNGCTG
CAAGCTGGAGGTGCCAGATTGACCGTGGTGGTGACGGTATCAACGACCTCCGGCCTTAGCGGCCGCGCATGTCGCAT
CGCCATGGGCGAGCCCCGAC (SEQ ID NO. 279)

Clone Rv255

.....Rv255SP6.seq:.....
GCACGCAATCGAAGTCACCCAAACCGGGCGGGCCAGGCGTCTNACGCCACGTNACCAGCCGCAACCTCAACCCGGCC
ACGGCGAGCTCCTGATCAAGGCCGAGGCCATCGGTGTCTACTTCATCGACACCTACTTCCGCTCCGGGCAATATCCGC
CGCAACTCCCGTTCGTTCATCTGCTCCGAAGTATGCGGCACGGTGGANGCCGTGCGCCAGGGGTTAC

(SEQ ID NO. 280)

.....Rv255T7.seq:.....

TCGACTGTGTGGCCACAGATCACGCCCCGCATGCCGAGCACGAGAAATGCGTCGAATTCGCCGCGGGCCGGCCGGCAT
GCTCGGGTTGCAGACGGCATTGTCGGTGGTGGTGCATACAATGGTGGCGCCGGCTTGTTGANTTNGGCGCGATATCGC
GCGGGTGATGAGTGANAACCGCGTGCA (SEQ ID NO. 281)

Clone Rv257

.....Rv257SP6.seq:.....

GAACCTGACACCCTGGTCACGGGTGAGCACGGACTTGATTTCTTCNCTATTGGTCGGCGCTGTTGAGCACACCACGCC
GCTGACGGCCGTCGCGTCTCGCTGTGCTCGGTCTGGTGGAGCGCGCTGCCCGGGCCNAACATCNTAAATCAAGCGT
ATTCGTCAACAGATATCATCAATGTCGGCGCTGGACTATTCAAATCATCGATATACTGGTGACCTGGTCTTCGCCAT
CGATCAATGGCGATAGTCACGCAAATCGTCACGGACATCGTCGGCGTCCCAGCTGGCCCGTCCCAACAGATGCTGCAA
CCCATCGGGGTGGTATCACCGCGGTGCTCGGCGATGGTCCACAATTCTTGCGGTCCAAGCCCNAAACATCCCGGGCAT
GAATTCACCGGCATGCGCN (SEQ ID NO. 282)

.....Rv257T7.seq:.....

CTATCGTACCCGCGCCGGTCACCTTCTGGATATCGCCGGCCTGGTCAAGGGGGCGTCCGAGGGAGCCGGGCTGGGTNA
CAAGTTCCTGGCTCATATCCGCGAATGCGACGCCATTTGTGAGGTGGTGGGGTGTTCGTGACGACGACGCTGACTCA
TGTACCCGGACGGGTCGATCCCCAGTCCGACATTGAGGTGTCGAGACCGAGCTGATCCTGGCAGATCTGCAAAACCT
GGAGCGGGCCACGGGCCGGCTGGAGAATGAAGCGCGCACCAACAAGGCGCGCAAGCCGGTCTACGAAGCGGCACTGCG
TGCCAGCANGTGCTCGACGCCGGGCAAGACGCTGTTGCGCGGGGGTGGATGCCGCCGCGTTGCGCGACTGAAACT
GCTGACCACCAAGCCCTTCCTGT (SEQ ID NO. 283)

Clone Rv258

.....Rv258SP6.seq:.....

TACTCAAGCTTCAGGCCGCCACGTCCGCCGTCCGTGCGCGACGTGACCTCGAGCGCCGAGTTCGACTCGACATCGCCG
CCGGCGCATGCCGACATGAACGCGGCACTCACCGCAAGCCCGTCGGACGTGAGTCGATCGACTCCGCTTCAAGCACC
GGATCGTCCGGGCACTCGCGGCCCTCGGCCTGTGCGAACGGCACACCCGTCGTGGCGGCNCCCCGCGCGGAAGTGGG
TCATCACGGTCGTTGCGAGCCGGTCGCGTCACCGCGTACCGACGCCGTC. (SEQ ID NO. 284)

.....Rv258T7.seq:.....

CCGACATCGAGTGGGCTCGCAGTGACTTGCGGACCTCCAAGCCACCGGTACCCGCCGCGCGGCAAGCCAAGGACGACG
ACGGCCTTGCCGATAGCTGCGCCAGGCGTTGCGCCAACTGGCGTCCAGCGTCGCCACGATCGTCAAAGAGCTTCATC
TGCCGAGTGTGTGCCATCTCATGGCTCCAAATATGGAATTAGGTCCCTGGGCGACTGACGACAGTCCCTCAGCGAC
CGGATTGCGCATCCCGCCTTGACGCTACTCCGCAAATCCCGGGCTTGCCTCCGCGGAAGCGAACTCGGCGGGCGCTAC
GTGGTGGTTCACTTCGGCCGTGCGCACTCGGATCGACGGGCCGATGGTGGCCGGGCCCGCGCGCTTCTTGGTCATCCG
ATTGAGT. (SEQ ID NO. 285)

Clone Rv259

.....Rv259SP6.seq:.....

ATACTCAAGCTTGTGCGGTAAACCGCACGCAGGGCGGTGGGTGCGGTGTCAAAGACACCCACACTTCTTTGCGGTTTC
GGTGATCTCGACACCGGCCGCGAGCCGACCACTGCGCGCGTAGATCGGCGATCAGCGCGTCGGCTATCGCCTGGGT
GCCGCCACCGGAATCGGCCAGCCGACCGAATGGGCCAGCGTTGCCAGCATCAGTCCGGCGCCGCGACACCACTGA
CGGCAACGGTGAAATCGCGTGGGCGGCAACGCCGTTGAACAACGCGCGGCATCCTCGCCCGCCAACGACCGCCAGGC
AGGGTGCCTGGGCCATCATCCGAGCCCGA (SEQ ID NO. 286)

.....Rv259T7.seq:.....

TGGAATCATAACGATCGGGTCAGCGACGCGCCAACACGAACGGCCGGACGAGTGGGCCAGGGTCGCGCCTCCCCTACA
AACAGGATCCGTTGCTTGCAGCGACAGGCTCCGGTGGCGCGTTGGGCGCCGTGCTCGTCCGAGCGTCGGGTCCCGGG
TCGCCGGCGACGCTTGTTCCTCCATACTCGCCCCCTAATCTCGAGGCGACCCGTACCCGCGAGCAACCTCCCAAAA
TGCAATCCCCCAAATGCAATGCGTCGAGCTATTCTCACACCGACCGTAGTTGCGGATCAGAAATCCGTTGGGCGC
GGAAGTCCAGCCGAATTTGTTCTCCCGCTCCGCATCATGCTTGTAATCGTTTGAAATCATCTCATATGCCTCGATC
GCTTCATAGGTCAAGCCCAAACCCGGCAGGATGGGTGGCC (SEQ ID NO. 287)

Clone Rv25

.....Rv25SP6.seq:.....

CTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATG
ACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTAGTGGTTGCGCACGTAAATTCGTCAGGT
GACCGATCCCCTGCTGTCTCACTCGCCTCACAGCGACCAACACGGCTGGCGCTCAAGCGGGGACGTCGCGAGCAGAT

GAGGAATGTGCGACGTCTTGATGCAGCCTGTCAGAACACCGAGACCCTCGACGAACTTACGATCGAAACCGCTTAGGC
CAACCGGTGACGGGGGTGTCTTCCGCGGCTAGGGCGCCTTATCGTCCGAAGGCCGTGGGTGGTATCGCCTTCTGGG
TCGCGCTTGGGGTCTGCTTGGCCGACGGTGCCGTCCCTGGACCGATCTCCAGCGGCATCCAGTGGCGATTCTGCC
ATCGG (SEQ ID NO. 288)

.....Rv25T7.seq:.....
CAGGCATGCAAGCTTGCGATGTATCAACACGCCGTTGCGCAGCGTGAGCCGATAGTTGACATCCGGCTCGGTGAAGGT
GAAATCGATGGCCAGGTGAGGTCCCATGCGCGTGGGCCATTGATGCTGATCGCCAGGACGTCAAAGATTGGTCCGG
CGTCAGCTGGGCGAAAAACGTGGGCGCCGGGACTTGCCCGGAGCTGCCCGGGTTCCTGCGCAGCTCGGCGGCCCC
GGTCAGAAAGAAATTGCGCCAGGTGCGCACTCCGCGCCGTAGGCCAGCTGCTCCACGGTGTGCGCATATAGCCCGCG
GGCCGACGCTGCTCGCTGTGCGCGAACACCGCATGGTCGAGAAGCGTTGCCGCCAACCGGAAATCACTGCGTCAAAG
CTTCGCCGGGCCACTCCAGCACTCCGTC (SEQ ID NO. 289)

Clone Rv260

.....Rv260SP6.seq:.....
ATACTCAAGCTTGACCGACGCTGATCGCACCGCACGGGAACCTCAAGGGCACTACTGGCACAAGGGCCACACGTC
AACCTGTAACTCCTGCGCCGACCCCGCCGAAGTCCTTGGCGTTAACACCGAACGGGCCAACCCGGGAATTTGGGT
CCATCAAAACAAATAGCAGGTGCCTGGGCGAGTGTTT (SEQ ID NO. 290)

.....Rv260T7.seq:.....
GTCGTGCTGTGCTGGGCGTCCGTATCAGCACGCCACGAAATGGGGCACAAGAAGGATTCCTGGAACGGTGGCTGTC
CAAGATCACCTCGCCCAAACTGCTACGGGCACTTCTACATCGAGCACAAACCGTGGCCATCACGTCCGCGGTGTCCA
CACCGGGAGG (SEQ ID NO. 291)

Clone Rv261

.....Rv261SP6w.seq:.....
ATATGCCTTGCTGAGCTTTTCGGATCGCAGCGAGTCGTACCCGCGCCGGTCACTTCGTGGATATCGCCGGCCTGGTC
AAGGGGGCGTCCGAGGGAGCCGGGCTGGGTAACAAGTTCTTGGCTCATATCCGCGAATGCGACGCCATTGTGAGGTG
GTGCGGGTGTTCGTGCAACGACGTGACTCATGTACCGGACGGGTCGATCCCCAGTCCGACATTGAGGTCTGTCGAG
ACCGAGCTGATCCTGGCAGATCTGCAAGCCCTGGAGCGGGCCACGGGGCGGCTNGAA (SEQ ID NO. 292)

.....Rv261T7.seq:.....
GACACCCTGGTCACGGGTGAGCAGGACTCGATTCTTCGCTATTGGTTCGGCGCTGTTGAGGCACAGCACGCCGCTGAG
GCCGTGCGTCTCGCTGTGCTCGGTCTGGTGGAGCGCGCTGCCCGCGGCCGAACATCGTAAATCAAGCGTATTCTGTC
AACAGATATCATCAATGTGCGCGCTGGACTATTCAAATCATCGATATACTGGTGACCTGGTCTTCGCCATCGATCAA
TGGCGATAGTCACGCAGATCGTCACGGACATCGTTCGCTCCAGCTGGCCCGTGCCAAACAGATGCTGCAACCCATCG
GGGTGGTATCNCGCGGTGCTCGGCGATGGTCCAACAATTCTTGGCGGTCCAAGCCGAAACCATCCGGCCATGAGTTC
ACCGGCATGGCGCAACGGCTGGTCCGGGGCAAACGCGGCGCGATCGAATTC (SEQ ID NO. 293)

Clone Rv262

.....Rv262SP6.seq:.....
TGTAAGGTGGGTCCCGTCCAATTCGCGGCGGGCGCGGATATGCCTTGCTGGTCTTGCTCATTTGATATCCAATC
TATGGGTGCTGGTTACTCAACGGGCCGAAGCTGGCCCTCCACGGGTAGGGTCTATTTCGACGGTGTATGCC
(SEQ ID NO. 294)

.....Rv262T7.seq:.....
CCCGAATCCGGTGGCCGGCAGGGGGCTGGCGACGTGGACACCTTCTAACTTGTCTTTACCGGTCACTGTTGCACCCC
AACACCTTTAACGACGTGGACGGACGTACATCGGATTCGACGGTGTATCCACAGCGTTGCCATTGGGCACACCCAC
TACGCCAATTTCTCCGACTGGGACACCTACCGCAGCCTCGCCCCACTGCAGGGACTGTTGTTCCCGCAACGGGCCATC
GACATGATCCAGTCTGGTGACCGACGCGGAGCAGACTGGTGCGTATCCGCGTTGGGCGCTGGCGAAATTCCGCCAC
CGGCATGAT (SEQ ID NO. 295)

Clone Rv263

.....Rv263SP6.seq:.....
TTGAGATGCTGGTCGGGATGCCGATGGTTGGAACATGGTCCCCTGGCGTCGAATACGCGCGAGCGCATGAGCTCACCG
GTTCCGAACAACGTATCGAAGAACTCGCACTGCTGGCAGATGGTATCTCCGATGTGGTTGTAATTTGTATCCCAACTC
TAACTGTGCTATCGGATCTGCGTGAATA (SEQ ID NO. 296)

Table 3 : End-sequences of the polynucleotide inserts cloned in the named recombinant BAC vectors contained in the I-1945 *M. tuberculosis* H37Rv genomic DNA library.

RvXXXSP6 corresponds to the SP6 end-sequence of the clone RvXXX.

RvXXXT7 corresponds to the T7 end-sequence of the clone RvXXX.

RvXXXIS 1081 corresponds to a region located close to a copy of the IS1081 repetitive sequence (Insertion element).

The character « - » denotes an uncertain base residue.

Clone Rv101

.....Rv101SP6.seq.....
 AATACTCAAGCTTGCCCGATGACAAAGAAATATGTCCGCAAAAGACTCAGCGGCCGACTTTGCTCGCAGCTG
 GCGGTACCGCGCCACCGATTCTATGCCGTGGTCGCGGAAAAATGCCTCCCGAAATCGCACGGCCGACTCCAGTTCGGC
 GAGCATCCGCGATGCCAGCTGCGGCTGCGCCTGCCGGCCACGGCACCCACATGCGGCAGTTCGTCCACCTGGGCCAG
 CGCCCCGCGCCGAATTCCAAACAATAGAACTGCACCCGGCCCGCATCGTGGGTAACAGCCAACGCCATGATCAGCGT
 CCGCAGCGCGGTTGACTTGCCCGTTTGGCGTGCACCTACGAACGCGACATTGCCTGCGGCCCCGACAAGTCGATCGT
 CGCGGCCACCCGTGACTGCTCTAACGGGCGATTGAAATTCCGAT (SEQ ID NO. 6)

.....Rv101T7.seq.....
 CCACCCGTGTAATTTGGGATGGGCAAAAAGGCGAAGCACCGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGG
 TTAGGGCTTCTCGCGGGAAGGCCCCGAACGTACGGCGTTTCAACACCTCGCGTCGCCCTCCGACCGCGAACATTCTGGG
 ATGGCAGCAACCTGCTGGCACCCTGGCGGGCGATGATCTGCAGCGTCGCCGCGGTAGTCGCCGCCCCGGGCGGCTAC
 ACTCTGAAACGCGATGACCATCGATGTGTGGATGCAGCATCCCGACGCAACGGTTCCTACACCGCGATATGTTGCGCT
 CGCTGCCCCGGTGGACCGGT (SEQ ID NO. 7)

Clone Rv102

.....Rv102SP6.seq.....
 AATACTCAAGCTTTCCGCGATACCGCCATGTGCGGCACATCCAGGACTTCTGGGGGATCCGCTGACAGCGGCGGG
 ATCCCAAAGTGCGGATGATCGGGCCGCCTACGTCGTGGTGACCTCGTCGGTAACAACGAAACCGAAGCGTATGACTC
 GGTCCACGCGGTGCGGCACATGGTGGACACCACCGCCACCGCACGGGTGAAGGCCTATGTACCGGTCCGGCAGC
 ACTCAATGCCGACAGGCCGAGGGCGGAGACAAAAGTATCGCTAAGGTACCGCGATCACCACATGGTGATCGCAGC
 AATGTTGCTAGTGATCTATCGCTCCGTAATTACCGCGGTTCT (SEQ ID NO. 8)

.....Rv102T7.seq.....
 GTGCCGTTCAACCCGAATTGGCTTTCCGCGCCATCGGTGAGGACGGCGTGCGGGTGCTCAACGACGACGTCGTCCGC
 GGGACACACCTCGATGCTGCCCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGC
 TTCCGCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTATGACGGCATCGCCACCGGAGCG
 ACGGCCAAGGCGGCGTGCCAGGTGCGCCGGGCGCACGGTGCGGACAAGTGCTGCGGGTCCCGATCGGCCAGAGC
 GACATCGTGGCGAGATTGCGCGGGTACGCCGATGAGGTGGT (SEQ ID NO. 9)

Clone Rv103

.....Rv103SP6.seq.....
 AATACTCAAGCTTTCCGCGGAAACGGACACATTGCGAATATTGATGACAAAATAAAAATCATTGATGGTTTGAGTCAC
 CAGGCCGATCAAGCCTTCGCCGAGCCAAATTCGAATCAAGAGGCCCAAGCCGTACCAATCAGCCCGCAACGAGGGA
 TTCCGTCAATTATCAGCCAAAATAACTGCTCTCGGGTACACCCAAACAGCGCAATATGGCGAAAAACGGTCGCCGTTG
 CACGACATTAAATGTCAGGTATTGTAGATTAAAAAGATACCCAC (SEQ ID NO. 10)

.....Rv103T7.seq.....
 TGCTCCCGAAACCTGGGGGTGTCCTGCTCTGTATGCACGGCATACGGACATCCTTCCCCTGAGACCCGCGGTGCAAC
 CAGCCACGTGTCCATCATAGNGGTCAACCCCGGCCAAGGGCGACGGCACGCCAAGTTTCGCCGACCGTTAACCTAGTG
 CTGTTAGCTTCAATTGCTGCGATCAAAACAGCTGGTCGGCGTTAGGAACTGAATTGAACTCAACCGATTGTTGGTGCC
 GCCGTAGGTGTCCTGGCTGCGGGTGCGCTGGTGTGTCGCGGTGTGGTAACGACGACAATGTGACCGGGGAGGTGCA
 ACCACTGGCCAGGCGTCGGCAAGGTGATTGCGGGGGGAAGAAGACACTCAAAGCCAGTGGGT (SEQ ID NO. 11)

Clone Rv104

.....:Rv104SP6.seq:.....
ATACTCAAGCTTTGCCGACGAGCGGGCGATGTTGATGACGGGAAACCCAGCGCACAACCGACGATTTTGGCGTAGCC
GGCGGACGTCTGCTCGATTCCGATCACGTGCGCGCTCGCATCGAGCATGGCGCCGGCGACGGCTAGCAGCGATCCGCC
GTCGTGAGGAGCAGACACGAGCCGTACGCCCGGCCGTAAGCCGCCCCAGGATTCGGCGAAAAACCGTTCTACGTG
GCGGGTGTACTGGGTGTGCAATGATTCTGTGGGGTGCCTAGGCGTGCCTGCAATCGTCGACATAGATGCCGTGCGGCCG
CATCGCTGCACAACCTCCGGGTGAGTGGAATAGCACTTGCCGATCACCGCCGACGTTGCGCGGATGAGGCCGAACCCGA
ATA (SEQ ID NO. 12)

.....:Rv104T7.seq:.....
TCCTATGTCCTGCCGAGCANGTGATCGAACGCGGTGACAGATTTGTCTATCCTGGACCTGACGGTGAGGTGCAAGTT
TTCCAGGAATTCGGCAAAATCGGTAAGAGCCTGAAGAATTCCGTATCGCCGGACGAAATCTGCGACGCATACGGGGGC
ATATACGCTTCGGGTTTACGAGATGTCGATGGGGCCGCTGGAGGCTTCACGTCCATGGGCCACAAAGGATGTTGTCGG
CGCGTACCGTTTTCTGCAGCGGGTGTGGCGCTTGCTCG (SEQ ID NO. 13)

Clone Rv105

.....:Rv105SP6.seq:.....
ATACTCAAGCTTGATTCCGCCGAAACCGACCGTGAGCACCCCGCCAGCCACCACGCTCGGGTCGGGCGCCGGGCCCCG
GCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCCGCGACACCACCCGGCTGCGCTACGTCTAACCATTCAGGGC
GAGGTACATCAGCTCGGCCGCCAGTGTTGCGGCCCTCTTTCCAGGTCGAAGTCTATACCGATATGCGCATCCGCAGC
CGCCACCCTGGAGAACAGAACGATGCCCTACTAATGCTTGTCTGGCGGGGCC (SEQ ID NO. 14)

.....:Rv105T7.seq:.....
GGTACGCTTCGGTCGCAGTCTGCGAGTGATGCATGACGACCGGGACCTCGTCGGCATCTTCCATAGCCGCCACACCT
TCAGTTGCTCACCGGAATCCAACCGGTAGAAGGTCGGCGAGCGCTCGGCATTGGTCATCGGGATATGCCGCTCGGGAC
GGTCAGAGCCCTCGGGTCCGGCCAGCACTCCGCAGGCTTCGTGCGGGTGGTCGCGACGCGCATGGGCCACCATCGCAT
TCACCAGGTCTGCGCGAATCACCAGCACGTAGACGGTTCTTTCTAAGCAACACCGAAGTTTCAGGACCGGAATGCT
CCGGGAACATGTCACGGTAGGTCGGTATTCCGGCTACCGGCTGA (SEQ ID NO. 15)

Clone Rv106

.....:Rv106SP6.seq:.....
GGCGTCAACGGTGTCGGAACCCGCTCAAGCAATTGGTAGGCCTGCAGTCTGTGAATCAGGCCGACGCTGTGGCCGCC
GCGGC (SEQ ID NO. 16)

.....:Rv106T7.seq:.....
GGCTNGCGTACCCGGTACCGGCCCGGGCCTACCACGTGCCGGAACCTGGAAGCGCAGTAAGCCCTCAACGCGCCACCG
CTTTGGCCCGCGCGCCCGCGGTAGGCGCATCGCGGTTGGCGTGGGGCGGCGCACTGCGACCTCACCAGCGGCTTTCCG
AGCTTTGTTGATCAACCGGCCAGCATGGTCGANGATGCATTGAGACCATATTCGAAATTGGTTTCATCGGGGGCCC
CGATCCGATGCCCCCTCCAGTTGCGTGAGCAANCAGCGGAGTCNTCGCGGGATCGATGGCCACGGGGTGTCAATGG
CGGATGGTCCGCTGCCCGCCGACTGGCTCTTGCGGGAGAACCGATCTAGCACCACCGATCCGCGCACGTNG
(SEQ ID NO. 17)

Clone Rv107

.....:Rv107T7D4.seq:.....
CGTAATNTCGCGACANCCANGACTTCTGGGGGGATCNGCTGACAGTGGTNGGATCCCAAATTGCGGATGATCGGGCC
GCCNACGTCGTTGTGTACCTCNCNTGTCACAACNAANCCGAANCGTATGACTCGGTCCACGCGGTGCGGCACATGGTG
GACACCACACCGCCACCGCNCGGGGTGAAGGCCTATGTACCGGTCCGGCAACTCAATGCCGACCGAGCCGANGCC
GGACACANAGTATCNCATAACGTACCCGCGATCACGAGCATGGTGATCGNNCAATGTTNCTANTGATCTATCGCTCCG
TAATTACCGCGGTTCTCGTCTTGATCATGGTCGCANCGAACTCCGGCGCAATCCGCGGATTTCATCGNCTTGCTCGCCG
ATCACATATTTTCAGCCTTTCACATTGCAACNAACCTGCTCGTCTCATGGNGATGGGGCGACACGACTACCGATATC
ATGCTCGCCGTTACACAATCNCGCCACGCCGCAAGACNGGAAACGCTTCTACACAATNTTNCNGGGACGCCACTNAA
CTTGTTTCNGGTTTGACATTGCCGCGCATGNTGCCAGCTTGCCGGCTCCCTTA (SEQ ID NO. 18)

Clone Rv108

.....:Rv108T7D4.seq:.....
TGAATTTCCCGATCCCAATCTCGGTTGAGATACAGGTCGCCATACCCCTTACTTCGGCAACGCTGGGCGGATTGGC
CCTGCNGTGCAGCANACCATCGACGCCATCGAATTGCCGGCAATCTCGTTCAGCCAATCCATACCCATCGACATTCC
GCCGATCGACATCCCGGCCTTCNCCCTTTAACGG (SEQ ID NO. 19)

Clone Rv109

.....Rv109SP6.seq:.....
AACAGCTATGACCATGNTTACGCCAAGCTATTTAGGTAACACTATANAATACTCAAGCTTTTACGGTGATCGCGCATC
ACCTGGTTCATGAACTGGAAGCAGCGCANCCTTCTTTTCGGCCGCAACATGAGCCAGCCTCTCGTCCGCGGTCTCGG
TGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCCTGAAACCAGCTTCCATATCCCGCGACNAACNACNCC
AGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCTTCTCCACCGACCGGGCCCGGGTGTGGGGTGT
TTCCGGCGACCGGCAGGTCAGGTGGTCCACACTGCCGACGGGCGCCGAGCCGTTACCGACCAAGCCGCCGAACAAGT
CCGCCCCGATCGCATACTCCAACCGGTTGCGGTACTGCAGGTGAGTGGCGTACCTCCTCNCGCTCGGCGAAGTCT
TGCTCCANACGTCGCGAGAACGGCAAGGAACACGTTCA (SEQ ID NO. 20)

.....Rv109T7.seq:.....
GACCGNNCCATGTTCCACAATGTGGTGCCAGTNCGGNGGCTACGTGCCATCNANACACTGGCGCAGGCTATCGCACC
CGTTATCNGCTACGAACAAATCNCGGTATGCGTTCTTTANCATGAGTCGGCGACCGNCGATCATGGTTCGACACCCACG
ACNGAAATACGCAGATCGCCNTCNAGCNTGTGTGCCGCGGATTATCANGACTGACCTCCTGGCTGACCGGNNTGTNTG
GTCCGCGATGCTTGGCGCCCGGCCGCGTGTGTCGTGGTTCGGCTCGGATAGCGAAGTCAGCTAATTCTCGTGGCAGCTCG
AAAGGGTCTTGGCGGTGCCGGTCTTTGCGCAAACCATGCNATGTTACGGTCCCTCGGGTGGCGCTGGCGGCGGC
(SEQ ID NO. 21)

Clone Rv10

.....Rv10SP6D2.seq:.....
GGGATGGGCGGGCCGCTAAACTCTTCGTGTTCCACTAACTCCGGGAGGGNCAATCTCGGGCCGTTATGGCTCACGTC
GCGTCGCCCTCCGACCGCAACATTCCGAGTTGGCAGCAACCTGGTAGCACCTGGCCGG (SEQ ID NO. 22)

.....Rv10T7D4.seq:.....
NCCGTCGTTGACAAGTAAATATGTCCGAAAAGTCTCAGCGGCCGACTTTGCTCGCAGGTGGCGGTACCGCGCCACCG
AGTCGATGCCGTGGTTCGCGGAAGAATGCCTCCCGAAATCGCACGGCTTCCCNNTTTAAACGGA (SEQ ID NO. 23)

Clone Rv110

.....Rv110SP6.seq:.....
TTTAGGTGACACTATAGAATACTCAAGCTTTTGGTCTAGCCGGCCGAGCAGGATACGGGTGTCATTGGCCACCGGCGG
CGGCTGTCCGGGAAATGGCGGGTCCCCGGTGGTTTGTCTGATGAGTGCTGAACCGTANTCGAAGTGGGCGGCGTCAGA
CTCCACCCANCCAGCAGGCAGCGCGAAGCTGAATCCTCCAACCGGGTGTGTCNATCCGGACAAGTTGGGGTGCCTTTGG
GGCAATGACAGGTGGCNGCGGTGCGTTCGGGTCCGCCGGCGGAAGTGCTGCGTTGGGATCNCCTGGGCTGGGCATTCCGG
NTTTTTCGGCGGGCGGTGGTNGGGGGGCAACAGGTNTCCNNGTGGGGTGGCGCTCAACGGTCNACGGCGCAAGCCG
CCGTTGTTGGTACCNGGGGCGCTGGCTCCGGATCGCGTTGGCGGTCCNCCG (SEQ ID NO. 24)

.....Rv110T7.seq:.....
CTACACCATCGAATACGACGGCGTCCGCCNACTTTCGGCGGTACCGCTCAACTTTGTGTCGACCCTCAACGCCATTGC
CGGCACCTACTACGTGCACTCCAATACTTTCATCCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATAC
GGTCGGTCCCAGATGACCCAGTACTACATCATTCGACCGGANAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCC
GATCGTGGGGAACCCACTGGCGAACCTGGTTCAACCAAATGANGTGATTGTTAACCTGGGCTACNGCGACCCGGC
CTATGGTTATTNACCTCNCGCCCAATGTTGCGACTCCGTTGGGTTGTTCCANAAGTCNNCCGGTTCGTCATCGC
CGAANCTCTCNTCCGGGACCCACAGGGAATCNGCNATTTCCNCTACAAATCANCCACCTCCA (SEQ ID NO. 25)

Clone Rv111

.....Rv111T7.seq:.....
GCATGATCGGCCACCTTTCGGGCGCCCGGCATACGGCGGCGTACCGATCTCCGCGTCATACACCGCGGGTAATCGC
CGACGGTGCCGGTTCGCGAGCCGAAGGTGACGACTCTGATTGAATCGAGTTCCAGGTCCAGCGGGTGGCGCACCAACG
GCGCGAGCTCAACGACGTCATCNCGTTGTCGCTTTCTACGGTCACCGACCTGGTGACCGTAGTTCCNCCG
(SEQ ID NO. 26)

Clone Rv112

.....Rv112SP6.seq:.....
GACACTATAGAATACTCAAGCTTGCCAACCGCCAGCCTGCATCCGGCGGCGANCACTGCTCCGCCGACCACTACGAAC
CAACCTGCGGTGCCCAGGCCATTGACGATGTGCTGGTCCGGCGCCCGGAGTCCGCGCACCATCAACGCCGCGGGCACC
ACCANGGCGGCCCCACCTGCAAGCGGACGATCATTCGGCGCGGCTCACGGCGGGCGGGGCTCGAACANGCACAGCA
TCAACGTNGTCACCGGCCGTGACCGGCCCGCATCGTCACACCAACCAAGCCATTGCGCTCCTCCTCAACNGGGCGA
CCCGGCCCGCATCGTCACAGGNCTAAGGCCATTGCCGTCTCT (SEQ ID NO. 27)

.....Rv112T7.seq:.....

TCGGCGCCATCGGCACCTTCGAGGACCTGTATTTTCGACGCCGTGGCCNACCTGAGGTTGGCGGTGGACNAAGTGTGCA
CCCGGTTGATTTCGCTCGGCCTTGCCGGATGCCACCCNCGCCTGGTGGTTCGATCCGCNAANAGACAANTTGTGGTGGA
NGCTTCTGCTGCCTGCGACACCCACNACGTGGTGGCACCGGGCAGCTTTAGCTGGCATGTCCTGACCGCGCTGGCCGA
CNACTCCAGACNTTCCACNAANGGTGCGCNCNCCCAATGTNCCGNANTGTCTCCGGNTCCCTTTACCNCCCAATGGGCN
GNTTCCACNGGTTACGGGCCCCNTNCCGGCGGGTCTNCCTCCCAANTACCAAATACGCCCGACNTTCCGGA

(SEQ ID NO. 28)

Clone Rv113

:Rv113SP6.seq:::

ATACTCAAGCTTTTATGGTGATCGCGCATCACCTGGTTCATGAAGTGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCA
ACATGAGCCAGCCTCTCGTCGGCGGTGGGTGTCAGGTGCTCGGGCAGCTCGGCCGCGAACAGCCCGGCTTGAACCTG
AAAACNGCTTTTCATATCCCGCAGCAAAGAACGCCAGTTCCGCTACTTAACCCCTCCGCGAACCGTCCATGGACAA
CAGCGCGTTCTCCACCAACCGGGCCCGGT (SEQ ID NO. 29)

:Rv113T7.seq:::

TCGGCTCAGGCCGCGCTGCTGGTAGAGTCGTCGACCGGTGTCAGGTTTCGACAATGTGGTGCCGGTTTCGGCGGCTACGT
GCCATCGAGACACTGGCGCAGGCTATCGCACCCGTTATCGGCTACGAAGCAAATCGCGGTATGCGTTCTTGAGCATGA
GTCGGCGACCGTCTGTCATGGTCGACACCCACGACGGAAGACGCAGATCGCCGTCAAGCATGTGTGCCGCGGATTATC
AGGACTGACCTCCTGGCTGACCGGCATGTTTGGTCGCGATGCCTGGCGCCCGGGCGGCGTGGTCTGGTTCGGCTCGGA
TAGCGAGGTGACGCAATTCTCGTGGCAGCTCGAAAGGTCCTGCCGGTGCCGGTCTTTGCGCAAACAATAGCGCAGGT
TACGGTTCGCGCGGGGTGCGGCCTGGCGGCGGCC (SEQ ID NO. 30)

Clone Rv114

:Rv114SP6.seq:::

CAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTCGCGTCTACGCCGGCCCGGAGCATCCGCACAGCGCTCAGCA
GCCGGTTCCGTACGANCTCAAGCAGGTGGCGCAATGACCGAAACACCCAGCCCGCAAACCCGGCGGCCCGGCC
GGGCCCCGACAATCGTTCTGTTGGAGCGGCCCATCCANACCGTTGGCGCCGTAAGGANGCGGTGGTACGAATGCGG
CTGGTGCCCGGCACCGGCAAGTTCGACCTCAACGGCCGCGAGCTTGGANGACTACTTCCCAAACAAGGTGCACCAGCAG
TTGATCAAGGCACCCCTGGTCACCGTGGATCGGGTGAAAGTTTCGACATCTTTGCCACCTGGGCGGCGGCGGCCGT
CCGCTCAGGCCGGGCTGCCCTGGGTATCGCCGGGCATTGATTCTGGTATCCCCNGAAGAACC (SEQ ID NO. 31)

:Rv114T7.seq:::

CGGTTGGCCACCGCTTCGCGGTGCGCGCCCGTTCGACAATGACCGTGTCTGCTGCTGACCAACACGCGTCGGGCC
GAGCCAGCACCTCCAAGCCACCTCGCGCAGCACCATGCCGCGTCGGGGTTGACCACTGGCCACCCGTCACCACC
GCCAGGTCTCAAGGAAACGCCTTACGGCGGTACCGAAGTACGGCCCTTGACCGCGACCGCTTCAACGTCTTGCG
AATCGGTTGACGACCGCTCGCCAACGCTTCGCCCTCCACGTCTTCAGCCACGATCAGTAGTGGCTTACCCGTTCC
TGCAACCTTTTCAGCAATGGCAACAGATCGGGAAGCGANCTGATCTTGTCTTGGTGCN (SEQ ID NO. 32)

Clone Rv115

:Rv115SP6.seq:::

CCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTTTGGCTGGGTGCGCTTCGAATTCNGCGTGACCCGCTATGG
GTTGCANAGCGGCTGGCGCCGACACCCACTGGCCCGGGTGTTCGCCCCGAACCCGGATCATGGTGAGCGAAAA
GGANATTCNCCTGTTGATGCTGGGATTCGCCACGCCAAGGCATCTANCGATTACTCTCNCGGGTGGGAAAAGTGC
CCAATCCCCCTCCCTCCAATTTCCNAACAATCATTCGGTTCNCNCTCCGGTTGGNGGTAACCNCCAATAAAACC
CTGCCCCG (SEQ ID NO. 33)

:Rv115T7.seq:::

GCCCGCNCATGGCCAATCCCCGAAGACATCATTTGCCAGTGGCCGGGCGCTAACAGGTTCCAGCCCCCACCANTGCC
GCTCGAACATGCGGTGCAACCCATTTCGAGGCCGGCAGGGAAAGCACCAGGAAAGCGCAAAGGGTGCAGTTCCGCG
CCCAATAATGTCGTCGCAACCCAGATGCGCTCNAACCCNCCGGCAGTCAGCGCACCCGACGCGANGTCGAAAGAC
GTCTCAGCGCGCCCATGGGGTGCCAATCGGCACGGCAGGTATGCCGCGCGCAACCCGAGCGGTGGTGCATGCC
ACGGTCCGCANGANGCGCANACCCGCCAATGCCGAANCCACGAAACATCGGGCGCATCCACCTTCAACC

(SEQ ID NO. 34)

Clone Rv116

:Rv116SP6.seq:::

ATACTCAAGCTTGGCCAGCCGTCGATGACAAGAAATATGTCGCAAAAGACTCAGCGGCCGACTTTGCTCGCAGCTGG
CGGTACCGCGCCACCGAGTCGATGCCGTGGTTCGCGGAAGAATGCCTCCCGAATTTCGCACGGCCAATTCATTCCGGGA
AGCATCCGCAATGCCAGCTGCGGTTGCCCCCTGCCGGCCACGGCACCCACTTGCGGCATTGCGTCCACCTGGGCCAGC
GCCCGCGGCCAATTCCAAACAATAAAAATTGCACCCGGC (SEQ ID NO. 35)

.....Rv116T7.seq:.....
CCACCCGTGTATTTTGGGATGGGCAAAAAGGCGAAGCACCGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGG
CTAGGGCTTCTCGCGGGAAGGCCGAACGTACGGCGTTTCAACACGTGCGCTCGCCCTCCGACCGCGAACATTGCGGG
ATGGCAGCAACCTGGTAGCACCTGGCCGGGCGATGATCTGCAGCGTCGCCGCGGGTAGTCGCCGCCCGGGCGGCTAC
AGTCTGAAACGCGATGACCATCGATGTGTGGATGCAGCATCCGACGCAACGGTTCTACACGGCGATATGTTGCGCTC
CCTGCCCCGT (SEQ ID NO. 36)

Clone Rv117

.....Rv117SP6D2.seq:.....
CTGCCCATTGTTTGGGGACGCCGACCAGCCGATGCTGGAGGCCTACACGGCCCTTGGTGCGCTGGCCACGGCGACCGA
GCGGCTGCAACTGGGCGCGTTGGTGACCGGCAATACCTACCGCAGCCNGACCCCTNTCNCAANAGGATNTTGTTCGCC
GGACCCCNCTC (SEQ ID NO. 37)

.....Rv117T7D4.seq:.....
CCGACTTTCGCGGTACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCA
ACTTCATCCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACT
ACATCATTGCGACGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACC
TGGTTCAACCAAATTGAAGGTGATTGTTAACCTGGGCTACGCGACCGCCTTT (SEQ ID NO. 38)

Clone Rv118

.....Rv118SP6.seq:.....
ATACTCAAGCTTTGTACACCAAGTGTTCGACCAGGCGCTCCATCCGGCGAGTGGATACTCCCAGCAGGTAGCAGGT
CGCCACCACGCTGGTCAGTGCGCGTTCAGCTCGCTTGCGGCGCTGCAGCAGCCATTGCGGGAAATACCTGCCCTGGCG
CAGCTGGGGGATCCCAACTTCAATGGTTGCGGCACGGGTGTCAAATTCACGGTGGCGGTAGCCGTTGCCCTAATTGGA
CCGCTCATCGCTGCTTTCGCGGTACCCGCCCCGCACAGGGCTTCGGCTTCAGCCCCCATCAGGGCGGCAATAAACTT
CAAGAGCACC (SEQ ID NO. 39)

.....Rv118T7.seq:.....
GAGGCAGCTTCGCCGGCAATTCTACTAGCGAGAAGTCTGGCCCCGATACGGATCTGACCGAAGTCGCTGCGGTGCAGCC
CACCCTCATTGGCGATGGCGCCGACGATGGCGCCTGGACCGATCTTGTGCCGCTTGCCGACGGCGACGCGGTAGGTGG
TCAAGTCCGGTCTACGCTTGGGCCTTTGCGGACGGTCCCGACGCTGGTCGCGGTTGCGCGCGAAAGCGGCGGGTCGG
GTGCCATCAGGAATGCCTCACCGCCGCGGCACTGCACGGCCAGTGCCGCGGCGATGTCAGCCATCGGGACATCATGCT
CGCGTTCATACTCCTCGACCAGTCGGCGGAACAGCTCGATTCCCGGACCGCCAGCGCATTTGGTGATGGAATCGGCGA
ACTTGGCCACCCGCTGGGTGTTGACATCCTCGACGGTGGGCAATTGCGCCTCGGTAAGCTTTCGCCGCTAGCCTTTTC
ATC (SEQ ID NO. 40)

Clone Rv119

.....Rv119SP6.seq:.....
ATACTCAAGCTTCACTGACAAGGGACGAATTCGTGCGCCGCCTGTTGACTGGGTGGTGGCCGAGCTGGTCGCCACCA
CTCAGGCCGCGGTACGCGCGGTACCGGCGCGGGAGCAAATCGCGCGGGCATGGCCAATTCTTGCGGACCATCACCG
CAGACGCCCGCTTCGGACCCCTGCTGTCCACCACACAGTTGGCCAACGCATTAATCACCCGCAAGCTTGCGGAATCCA
CCGCCCTGTTGCG (SEQ ID NO. 41)

.....Rv119T7.seq:.....
TCCATCACCCGATGTGGCNGGAGCACTGCCATGTGATCTCAACTACCACCTCCGGCCGTGGCGGTTGCGCGCCCCGG
GGGTTCCGCGCGAACTCGACGAGGCGGTGCGGAGAAATCGCCNACCCCGCTGAACCGCGACCCCGCTGTGGGAGA
TGTACTTCGTTGAGGGGCTTGCCAACCACCGGATCGCGGTGGTTGCCAAAATTACCATGCGTTGGCTGACGGTGTG
CCTCGGCAACATGATGGCACGGGGATGGATCTGCCGCCGGGACCGGAGGTGCGCCGCTATGTGCTGACCCCGCTC
CTACCAAGCGGCA (SEQ ID NO. 42)

Clone Rv11

.....Rv11SP6.seq:.....
AGCTTTGCAGTTGCTGAGTAATGTCGGCCAACGTCACCACAACCGCGATGAATTCATCATGCCGCCAGGGCGGGCA
ACCAATGGTGGCCGCGAGCGGAGTCGATCGCAGCGGAGGTTGCCGGCCGAGTTGATTACGAACAGGGTGA
GGTCATAGGCGGGCAGGATAGTGACGAAGGCAAGACCTCCATCTGCCGTGCGGAAGAAGTATCGAG (SEQ ID NO. 43)

:::::::::::::Rv11T7.seq:::::::::::::
AGCTTCAGAACAGGCCTGTTGTGGGCGCACCCGGCTCGCCGAGTTCTGCACGCACCGCCTCAAGTGC GGCCCGCACCG
CCGGCATCTCCCGGTACAGCAGGGCCGCGGCCCGCGCCGACGACGGCGTGTTCGCGCAGTTCCCGTCAATGATGC
TGACCTGATCGGCCACCCGGGCGTTCTCGGCGTCGTCGCGTTCACTAATCGCGGTGCTCAGCAGCGTCTCGACAGCCA
CCACCCGAGTGCGGACACAGCTGCTCCACCACGGACCGCAGCGATGCCCGTC (SEQ ID NO. 44)

Clone Rv120

:::::::::::::Rv120SP6.seq:::::::::::::
ATACTCAAGCTTCAGTTCTCCACGACGCGTTCCCAAATGAATTTCCCGATCCCACAATCTCGGTTCAAGATACAGGTC
GCCATACCCCTTACTTCGGCAACGCTGGGCGGATTGGCCCTGCCGCTGCACCAAACCATCAACGCCTTCAAATTGCCG
GCAATCTCGTTCAAGCAATCCAT (SEQ ID NO. 45)

:::::::::::::Rv120T7.seq:::::::::::::
GCTCTACGCCGCTACGGGTGGAACATGCATCCCGAGCAGATGCTCGAGCGCGCACCCCACTCGCCGATGGCCGGAAC
CGGCTGGTTACCCGGGTGGCGGCTGACGTTCCGGCGCGAGGACATCNGCTGGGAAGGGGCGCTTGCCACCGTTCGTCTNA
AGACCCAAATTCGAAGGTGTTCTGTCGTGCTCTACGACATGACCCCGGCGGACGAGAAGAACCTTGACCGGTGGGAAGG
CTCCGAGTTCCGGTATCCACCAGAAGATCCGATGCCGCGTGGAGCGCATTTCTCGGACACCACAACGGGATCCCGTCC
TCG (SEQ ID NO. 46)

Clone Rv121

:::::::::::::Rv121SP6.seq:::::::::::::
ATACTCAAGCTTGCCAAAGAGACCTCGTCCACCAAGCAGGACGCGACCGTCGAGGTGGCGATCCGGCTTGCGGTGCGAC
CCGCGTAAGGCAAACAGATGGTTTCGCGGCACGGTCAACCTGCCACACCGGCACTGGTTAAGAACTGCCCGCGTTCGC
GGTTTTTCGCGGTTGGTGAAGGCCAATGCCGTGCGTTTGCCGTGGGGCGGATGTTGTGCGGAGTGACAATCTGATCA
AAAGGATTACGGGCGGTTGGCTGGAATTCATGCCGAATCGCGACACCGG (SEQ ID NO. 47)

:::::::::::::Rv121T7.seq:::::::::::::
CCACGGCGTGGATCAAGGTACCGGCCGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGCTTGATGTCGGCGTTAGCGC
CGGATTCACACATCCCTTGCGAAAGTCCGTTGGGTGCAATGATGTAGCGCTTCTCCCCATCGAGATAGTGGAGCA
ACGCAATCCGTGCGGTACGGTTCCGGTCTACTCGATGTGCGCGACCTTGGCGTTGACACCATCTTTGTCATTGCGGC
GAAAGTCGATCATCCGTAAGCGCGCTTATGACCGCCGCTTTGTGCCGGGTGGAATCCGGCCATGCGCGTTGCGTC
CACCGCGACGTGCAGCGGGCGCACACGAGCTTCTCCGGGGTTGACGGGTNATCTC (SEQ ID NO. 48)

Clone Rv122

:::::::::::::Rv122SP6D2.seq:::::::::::::
GCAGCATGACGGCGGTAGCGAACACCGCCGGATGCAGCGCAAGTAGCGTCGATGTGCTACGGAATCGCCCCGGCACC
GCGATCTCGANGATCACCAGTGCCACCCCTGCAGCGCNACACCGACGATTCCGTACACCGCCACGCCGATCAGGCCC
TGGGCCATCTGATTGGAGCTGGCGTANATGGCGGCGATGGTGACGATGGCCAGCGCCACATACATTGTGGCGGCCAGA
ACCACGGCGTTGGGGCGGCGGTGATGAACACTAGGCGACGCGATCGCCGGGGTCAACAGGTTGACCATCAGAAAG
CCTGCGACTAGCACGGCGGCGCCACTAGGAAGTACAAGAANGTGGCCACCACCCCATGCAGGATCGGGGTAAAGGCTGA
TGGTCCCGAAATCGACTCCGGCCTAATACATGACTCTCTCTTTGCGTCATCGCCTTACTTGTGCGCGGAA
(SEQ ID NO. 49)

Clone Rv

:::::::::::::Rv123SP6D2.seq:::::::::::::
GGGACACACCTCGATGCTGCCGCGNATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGC
TTCCGCGCGGGCGTGACGCATCCCGTTGACCGGCCGGANCTCTCTA (SEQ ID NO. 50)

:::::::::::::Rv123T7D4.seq:::::::::::::
TGGGCGCCTCTTTCCGCTTCCNNTTAAACGNAGCANGACATTCTGGGTATCGAGTTGTACTGGATGGTGTGGCG
ATGTGCGGTGATCCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCCGGTTGAAAGAGGAAATTGGG
GCCGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGAGTGGTGACGGCTGCCGGCATGGTGTTCGCC
GTTACCATGTGCTTGTGTTTACGCGATTGCGAATTATGGTTCAGATCGGTACCACCATCGCCTTCCC
(SEQ ID NO. 51)

Clone Rv124

:::::::::::::Rv124SP6D2.seq:::::::::::::
CCGATCGGCGCCGCANCTGGTTGGTGTTCGGATGAATCCGCAGCGAAAATGTAGCTGCGGTGGCGTGTGCTGACTCG
TNGGCGTCGACGCTCGTGGCAGCCACCGANCGGTTGGTCCAGGATCTGGATGGGCAAAGTTGTGCGGCCCGGCCGGT

ACGGCCGATGAGCTGACCGAGGTCGACAGCGCCGTGTTGGCTGACTTGAACCGACATGGAGTCGCCCCGGTTGGCGT
CACCTCAAGCATTTCAATGGTTATGCGACAGTTTGGGTTACGCCGTCAGACATCACGTCGGAGACTTGGATGAGC
TGTGTCTGCCAGATAGCCCCGAATCGGGACGACCGTGGTCACGGTGCGTCTGACCACTCGGGTCGGGTCGCCCCGCGT
ATCGGCATGGGTGCGTNATCACAGCGACGCGCCTGCCAAGGANGTNCGGNCGGACC (SEQ ID NO. 52)

::::::::::::Rv124T7D4.seq::::::::::::
CGGGTTGCGGATCCACGCGTGCGGGTTGTCAGCAGCTACGGCACTGAACCGCGCCACAGCTCGCCGATCCGCTTTTCG
GTGGTTCTCGATCGACTCGCCGTAGGCGATGCGCAGCGCCTGCTCGAATATCGGGTACACGTAGGCCGGCCTTCCNC
TTTA (SEQ ID NO. 53)

Clone Rv126

::::::::::::Rv126SP6.seq::::::::::::
CTTGATTTTGATCATCATGACGATCATCACCTAATTTTGTACCCGCACTGGTTATCGTGGGTACCGTCGTGCTTTC
CATGGGCGCCTCTTTCGGGCTTTCGTTATGGTCTGGCAGGACATTCTGGGTATCGATTGTACTGGATGGTGTGGC
GATGTCGGTGATCCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCCGGTTGAAAAGGAAATTGG
GGCCGGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGAGTGGTGACGGCTGCCGGCATGGTGT
(SEQ ID NO. 54)

::::::::::::Rv126T7.seq::::::::::::
GGGGATCCCTAGATCGACCTGCAGGCATGCAAGCTTGGCGTGCTTCCAACCCGAATTGGCTTTCGGCGCCATCGGT
GAGGCGGGACACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGG
AACGCTTCCGCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATCGCCACCG
GAGCNACTGTCAAGGCGCGTGCCAGGTCGCCCGGGCGCACGGTGCGGACAAGGTGGTGTGGCGGTCCCGATCGGCC
CAGACGACATCGTGGCGAGATTGNCGGGTACGCCGATGAGGTGGTGTGTTTGGCGACGCCGGGCTNGTTCTTCGCCG
NCGGGCANGGTTACCGCAACTTCAACCAGACCTCCGACGACGAGGTGGTGGCGTCTCTGGATCGTGCTC
(SEQ ID NO. 55)

Clone Rv127

::::::::::::Rv127SP6.seq::::::::::::
AAGGCTGCAGGTCGAAGCGGNTGGTTACGACTCCCTGTGTGTGATGGACCAGTTCTACTATCTGCGTCTACACGGCCC
TTGGTGCGCTGGCCACGGCGACCGAGCGCTGCAACTGGGCGCGTTGGTGACCGGCAATACCTACCGCAGCCCCGACC
CTGCTGGCAAAGATNATCACACGCTCGACGTGGTTAGCGCCGGTCGAGCGATCCTCGGCATTGGAGCCGGCGGGTTT
GAACTGGAACACCGCCAGCTCGGCTTCGAGTCCGGCACTTCCAGTGACCGGTTCAACCGGCTCGA (SEQ ID NO. 56)

::::::::::::Rv127T7.seq::::::::::::
CTTTCGGCGGTACCCGCTCAACTTTGTGTCGACCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAATACTT
CATCCTGACGCCGGAACAAATTGACGNGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACTACAT
CATTCGCACGGAGAACCTGCCGCTGTACAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGT
TCAACCAAATTGAAGGTGATTGTTAACCTGGGCTACGGCGACCCGGCCTATGGTTATTGACCTCGCCGNCCAATGT
TGCGACTCCGTTTCGGGTTGTTCCAGANGTCAGCCCGGTCGTCATCGCCGACGCTCTCGTCN (SEQ ID NO. 57)

Clone Rv128

::::::::::::Rv128SP6.seq::::::::::::
CGGTATAGCCCTCGGGTCCGGCCAGCACTCCGACGGCTTCGTGGGGTGGTCGCGACGCGCATGGGCCACCATCGCA
TTCACCAAGTTCGCGCAATCACAGCACGTAGACGGTTCTTTCTAAGCAACACCGAAGTTTCAGACCCGAATGC
TCCGGGAACATGTACGGTAGGTCGGTATTCGGGTACCGGCTGAGCATTGAGCACGCCGGCCAGCACCGCACGAGC
CAGGCAATCAGCCGCCCGCCGACCGATCGCGGTGACAGCTGAGTCTCCGGAGACAATGCGGCCGCGACCGCGNCTC
CGCGGCACCGCTACNGCGCCGTGG (SEQ ID NO. 58)

::::::::::::Rv128T7.seq::::::::::::
GTGATGGCAGCCACCGACACACCGGCTGCGTACNTCGAGCCATACCGGGCGGAGCTACATCGGCTCGGCCG
CCAGTGTTCCGGCCCTCTTTCGAGGTGAGGTGATACCGATTGCGCATCCGCANCCGNCCTGGACGACAGAACC
GTGCCCTACGAGTGCTTGTGGGCGGGGCCAAAGAACAGCTTGGCATCTGGCGCGATTGGCCGCGCGCGCTGGT
GCCAAGGACGACCGGTTCCGGTGTGATCGACGACGCGTGGGGTTACCGATCCGGAGCGACTATCAAGATGGGG
AGGTCTTGACACCATCGGCCCNACGGACATGTGATCGTCCGACGTGAGTCCACCCG (SEQ ID NO. 59)

Clone Rv129

::::::::::::Rv129SP6.seq::::::::::::
GCGAAAGTCCGTTGGGTGCAATGATGTAGCGCTTCTCCCATCGAGATAGTGGAGCAACGCAATCCGTGCGGTACGGT
TCGGGTGCTACTCGATGTGCGGACCTTGGCGTTGACACCATCTTTGTATTGCGGCGAAAGTCGATCATCCGGTNNG

CGCGCTTATGACCGCCGCTTTGTGCCGGGTGGTAATCCGGCCATGCGCGTTGCGTCCACCGCGACCGTGCAGCGGGC
GCACCGAGCGACTTCTCCGGGGTTGACCGGGTGATCTCGGCGAAATCAGATACGCTGGCGCCGCGACGACCGAGCGCTCG
TGGGCTTGTNCTTGCGAATTGNCATGTCTAATCANGTCTTTCTCTCAGCTCTCGTCGCGGGGCTAGGCCGCAATTGCC
CTGCTCCTCCTCATCGCTTCGCTCTGCATCGTCCCCGGGCTAAGCCCGTGCCCCGAAA (SEQ ID NO. 60)

::::::::::Rv129T7.seq::::::::::
GATGGTTGCGGGCAGGTCAACCTGCCACACGGCACTGGTAAGACTGCCCGCGTTCGCGGTATTGCGGGTTGGTGAAAA
GGCCGATGCTGCCGTTGCCGCGGGGGCGGATGTTGTGGGAGTGACGATCTGATCGAGAGGATTACAGGGCGGCTGGCT
GGAATTCGATGCCGCGATCGCGAACACCGGATCAGAATGGCCAAAGTCGGTCGCATCGCTCGGGTGCTGGGTCCGCGC
GGCCTGATGCCCAACCGAAAACCGGCACCGTCACCGCCGACTCCCCATGGCGTCCCGGATATCAAGGGCCGGCAAAT
CAACTTCCCGGTTGATCAGCAAGGCAACCTGCCTCNCCTCCGG (SEQ ID NO. 61)

Clone Rv130

::::::::::Rv130SP6.seq::::::::::
ATACTCAAGCTTCGTACATAAGACCATGGTGCGCTTTCTTTACCCCGTCCAGAGTCGGGGGCATCCGCACCGGCTCGCA
TCGCATCATCTCCACGACGGGCGCTCATCAGCTTGGGCCATTTCAATGTACTTGATAACCCGCGCTGCGGGTAGG
CCACTGCGACAATTCAAACACGGTGTACACGGTGAATAGTGTGAGATGGGCTCTGATCAACCGTCGCAAAACCGGT
TTCGCATCAATAGCGGAATCCACCGGTTGCATGGAGGCTGCTGACCTTGAAAACAAAATTTTTTCATTACAACAA
AACACCGCCNCGGAACTTTGCA (SEQ ID NO. 62)

::::::::::Rv130T7.seq::::::::::
CGAATTCGGCGTGACCGCTATGGGTTGCAGCAGCGGCTGGCGCCGCACACCCCACTGGCCCGGGTGTTTTCGCCCCG
AACCCGGATCATGGTGAGCGAAAAGGAGATTGCGCTGTTGATGCTGGGATTGCCACCGCGAGGCCATCGACCGATT
ACTCGCCACCGGGGTGCGAGAGGTGCCGAGTCCCCTCCGTGACGCTCTCCGACGATCCATCCGGCTTCGCGCGTCG
GGTGGCGGTAGCCGTGATGAAATCGCTGCCGGCGCTACCTGCAAGGTGATTCTGTCCCGTTGTGTGCAAGTGCCCTT
TCGCGATCGACTTTCCGTTGACCTACCGGCTGGGGCGTCGGCACAAACCCCGGTGAGGTCGTTTTTGTGAGTTGG
GCGGAATCCGTGCTCTGGGTTACAGCCCCGAATCGTCACGGCGGTGCGCGCCGACGGAGTTGTTATACCGATCCGT
TGGCGTACCGCGCCTTGGGC (SEQ ID NO. 63)

Clone Rv132

::::::::::Rv132SP6.seq::::::::::
TCAGACTCCACCCAGCCAGCAGCGCAGCGAAGCTGAATCCTCCAACCGGGTTGTCGATCCGGACAGGTTGGGGTGCG
TTTGGGGCAATGACAGGTGGCGGCGGTGCGTTCGGGTGCGCCGGCGGAGGTGCTGCGTTGGGATCGCCCGGCTGGGCA
TTTCNGCGTGTGGCGGCGGCGGTGGTGGGGGGCAACAGGTGTGCGCGGTGCGGGTGGCGTGCAGCGGTGACGGC
GGCGAAGCGGCGGTTGTGGGTACCGGGGGCGCTGCTCCGGATCGGCGTTGGCGGTGCGGGGACCGCAACGGTCACC
AAGCTGGCGCTGGCCATCGCCGCGATAGCCAGTGCCGCCAATCGTCCCTTGCGACGTGTCAAGTNGGGGTCCACCTGA
TGCATGGCCAAAGAACCTACCGTGTTAACGGCNCAACNCAAGGACCGCGCGGTGCGN (SEQ ID NO. 64)

::::::::::Rv132T7.seq::::::::::
TTTCCGCGGTACCGCTCACTTTGTGTNACCCTCAACGCCATTGCCGGCACCTACTACGTNCACTCCAACCTACTTC
ATCCTGACGCCGGAACAAATTGACGCGAGCGGGTCCGCTGAACAATTCGGTCCGTCCCACGAAAGAACAGTTTNCNT
CTTTCNCACGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGTG
TTTCAACCAACACTTAGAGTGAATTGTAACTGGGCTAGGGGAAACCGGCTCTAGTTTTTCCACNTCTCCGCCCC
NTGTTTCGAATACTCCGTTGCGGGTTGTCCCAAA (SEQ ID NO. 65)

Clone Rv134

::::::::::Rv134SP6.seq::::::::::
GCTTCGGGCTCGTATGTTGTGTGAATTGTACCGGATACCAATTTACACAGGAAACAGCTATGACCATGATTACGC
CAAGCTAGTTAGGTGACACTATAACAATACTCAAGCTTGCCGGTGGTGGGCGGACCACTTCGATGGCAGACCCGTGA
ACTGCTGCCCGGCCAATTCTTCTTGGTCGCGCGGACCGATGGACCGGCTGGGATTCCAGAAGGTGCCGATCCGCG
CCCTGGGAAAAACCGCTGCACCTCTACTTCACGACCAACGAC (SEQ ID NO. 66)

::::::::::Rv134T7.seq::::::::::
CCGATCGACTGATGCGCCGACAACACGCCCCAACAACTGGAATGAACCGTCGTGACCATCATCAGCACGCGGTTGTA
GGCGACTTGCGACATGTTCAACCCGCGTACTCGGACGGAATCTTCAAACCGAAACAGCCAGCTCGGCCAGGCCCTTT
CACGTAATCGTCGGGGATCTGGGCACCAAGCTCGAGGACGCTGCCGTCCACGGTGTCTAGGAATTCGCGAGTTTGAC
CAGAAACGCTCGGTTGCGGCCTCTCGGCGTCCGACGGCTGGGAAATGGGTGTATGAGCCCTACGGGAAACCGGCC
CACAAAGAGTTCTTTGGCGAAGGACGGTTATCCCAACCACTTTCGCGAGATTCTCGGCAAGGGCCCGCGCTTGCTC
CTCGGTGACCTGAGTTGTGTGCCATCGCCGCTCCTCCCTGA (SEQ ID NO. 67)

Clone Rv135

.....Rv135SP6.seq:.....
TGCATCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG
CCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTTACGGTGATCGCGCATCACCTGGTTCATGAACTGGAAGC
AGCGCAGCGCTTCCTTTTCGGCCGCAACATGAGCCAGCCTCTCGTCGGCGGTGCGGTGTCAGGTGCTCGGGCAGCTCGG
CCGCGACAGCCGCTGACCTGAAACCAGCTTCCATATCCCAGCAGAACGACGCCAGTCCGCTACGTAACCCCTCCG
CGACTGTCCATGGACAACAGCGCGTTCTCCACCGACCGGGCCCGGGTGTGGGGTGTTCGGCGACCGGCAGCCAGGTG
TCCACACTGCCGACGGGCGCCGCGAGCCGTTACCGACCGAGCCGCGAGCAAGTCCGCCCGATCGCATACTCC
(SEQ ID NO. 68)

.....Rv135T7.seq:.....
GGGGGCGCTGCTGGTATAGTCGCTGACCGGTGCAGGTTTCGACAATGTGGTGCCGGTTCGGCGGCTACGTGCCATCGA
GAACTGGCGCAGGCTATCGCACCCGTTATCGGCTACGAGCAAATCGCGGTATGCGTTCTTGAGCATGAGTCGGCGAC
CGTCGTGATGGTCGACACCCACGACGGAAGACGCAGATCGCCGTCAAGCATGTGTGCCGCGGATTATCAGGACTGAC
CTCCTGGCTGACCGGCATGTTTGGTCGCGATGCTGCGCCCCGGCCGGCGTGGTCGTGGTCGGCTCGGATAGCGAGGT
CAGCGAATTCGTGGCAGCTCGAAAGGGTCTGCCGGTGCCGGTCTTTGCGCAAACGATGGCGCAGGTTACGGTCGC
CGGGGTGCGGCTGCGGGCGGCCAGAGCACGAGTTACCGATGCGCAGCTAGTGGCGACAGCGTCAGCCAAC
(SEQ ID NO. 69)

Clone Rv136

.....Rv136SP6.seq:.....
TGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG
CCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTCCGTACAGGTCGCCTCCAACACGGCGGGGAAGCGACACCA
GCTACCGAGCTTGGAGTCCAGGACGCCAGCGCGCGCGTTCGGTCTGCGTGGTGCCGCCGGGTGGCGTTGGCTGG
CAACGATCTCCACCCAGCCGGTTCGGGTTACCCACGATCTCGGCATAGACCGGGCCGAGGCCGTTGCGATACCGTATT
GCGTCAATTGGGACGCGGTTGTGCATTGCGCTAGCTCGGTTGCCACACCCGTGAGGGGTTGACGTTGGCGGGTTCGG
CGGGCCCCAGCACCGCTGTCACCATGCCCGCAAGCCGACCTGCGGCGCCACCAACT (SEQ ID NO. 70)

.....Rv136T7.seq:.....
CGGCATGACCACCGACAGGCCCGACTGGTCGTACCACTCGAACGCCGGGGTGTGATGTCCCAGCCGCTGAAGTCGTC
CTGCGCGCGCAGGCCGTCGAGCAGGTACAGGGCGGGCGAGTTGGCACCACCACTTTGGAATTGGACCTTGATGTACG
GCCCATCGACGGCGACGGCACCTGCAGGTACTCCACCGGCAAGCCCGCGGGGAAATGCCCCCGGGTTCGCCGTGCC
ACCGACGGCGCCGACGACCCGACACTAGGGCCGCGCCGACGGCCCCGACCACGAGTCGACGCGACATACCCGTGAC
GGCGCCACGAACCTGTCAACAAGCTGCATTCTTGCTTCCCTCATCTCAACGCATCCATGCATGTTTGGGCG
CATCTGAATTANGTCAGACTGCAGGCGCTGGGCGGCGAGTGCTCGTGTATCAACCACAACCTTCGGGCGT
(SEQ ID NO. 71)

Clone Rv137

.....Rv137SP6.seq:.....
TTCCAACCCTAATTGGCTTTCGGCCCCATCCGTGAGGACGGGGTGCAGGTGCTCAACAACAACGTCGTCCGCGGGACA
CACCTCTATGCTGCCGCCATGGACGCGGTCCAACGCAAGCAGCTGATCGAGCTACAACCCCGCGCGGAACGCTTCCGC
CGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATCGCCACCGGAGCGACGCC
AAGGCGGCGTGCCACGTCGCCCGGGCGCACGGTGCGGACAAGGTGGTGCTGGCGGTCCGATCGGCCAAACGACATC
GTGGCGAGATTGCGCCGGTACGCCGATGAGGTGGTGTCTGCGCAGCGCGGCGTGTCTTCGCCCTCGGGCAGGGT
TACCGCAACTTCAC (SEQ ID NO. 72)

.....Rv137T7.seq:.....
CAGGCATGCAAGCTTTCCGCCGATACCCGCCATGTGCGGCACATCCAGGACTTCTGGGGGGATCCGCTGACAGCGGGC
GGATCCCAAAGTGCGGATGATCGGGCCGCTACGTCGTGGTGACCTCGTCGGTAACAACGAAACCGAAGCGTATGAC
TCGGTCCACGCGGTGCGGCACATGGTGGACACCACACCGCCACCGGCGTGAAGGCCTATGTACCGGTCGGCA
GCACTCAATGCCGACAGGCCGAGGCCGAGACAAAAGTATCGCTAAGGTACCGCCGATCACNAGCATGGTGATCGC
AGCAATGTTGCTAGTGATCTATCGCTCCGTAATTACCGCGGTTCGTCTTGATCATGGTCGGCATCGACTCGGCCAA
TCCGCGGATTTCATCGCCTTGCTCGCCGAACACAACATTTTACCTTTACATTTGACCAACCTGCTCTTCTCAT
(SEQ ID NO. 73)

Clone Rv138

.....Rv138SP6.seq:.....
CACTACTCAAGCTCTCTCATTACCACCCCTGTAATTTGGGATGGGCAAAAAGCGGAAGCACCGCTTGGCCACNAA
CGCCGGGAGGGACAATCTCGGGCGGCTATGGCTTCTCCGGGAAGGCCCAACGTACGGCGTTTCAACACGTCGCGTC
GCCCTCCGACCGCAACATTCGGGGATTGGCACCACCTGNTACCACCTGGCCGGGCGATGATCTGCAGCGTCGCCG
CGGGTAGTCCCGCGGGCGGCTACAGTCTGAAACCCCGATGACCATCGATGTGGATGCAGATCCGACGCAACG
GTTCTACACGGCGGATATGTTCTCTCGCTGCGCCGGTGGACCGGTGGGTCTATCCCTGAAACCGACATCCCN
(SEQ ID NO. 74)

.....Rv138T7.seq:.....
CAGGCATGCAAGCTTTTCGTGCTCAGTTCATTGCGCCAGCAGACCAACAAGAGCATCGGGACATACGGAGTCAACTACCCGG
CCAACGGTGATTTCTTGGCCGCCGCTGACGGCGCGAACGACGCCAGCGACCACATTGAGCAGATGGCCAGCGCGTGCC
GGGCCACGAGGTTGGTGCTCGGGCGGCTACTCCCAGGGTGCGGCCGCTGATCGACATCGTCACCGCCGCCACCACTGCCCG
GCCTCGGGTTACGCGAGCCGTTGCCGCCCGCAGCGGACGATCACATCGCCGCGATCGCCCTGTTTCGGGAATCCCTCGG
GCCGCGCTGGCGGGCTGATGAGCGCCCTGACCCCTCAATTGCGGTCCAAGAACATCAACCTCTGCAACAACGGCGACC
CATTTGTTTCGGACGGCAACCGGTGGCAACGCACCTAAGCTACTTGGCCGGGATGA (SEQ ID NO. 75)

Clone Rv139

.....Rv139SP6.seq:.....
GTTTATGCACTGGTTAGGTGTTCCATGAGTTTCATTCTGAACATCCTTTAATCATTGCTTTGCGTTTTTTTATTAAA
TCTTGCAATTTACTGCAAAGCAACAACAAAATCGCAAAGTCATCAAAAACCGCAAAGTTGTTTAAATAAGAGCAAC
ACGTACACAAGGAGATAAGAAGAGCACATACCTCAGTCACTTATTATCACTAGCGCCCCGCCGAGCCGTGTAACCGAG
CATAGCGAGCGAACTGGCGAGGAAGCAAGAAGAACTGTTCTGTGATAGCTCTTACGCTCAGCGCAAGAAGAAATA
TCCACCGTGGGGAAAACTCCAGGTAGAGGTAC (SEQ ID NO. 76)

Clone Rv13

.....Rv13SP6.seq:.....
ATACTCAAGCTTGGGTGTAGCCGATCACCAGGAGTCNCATGATCAGCCACGTTCCGCGCCGCCCGGCATACGGTGGTG
TACCGATCTCCGCTCATACACCCGCGGGTAATCGCCGACGGTGCCGCTTCGCGAGCCGAA (SEQ ID NO. 77)

.....Rv13T7.seq:.....
AGCTTTATCGAAAGCGCGAACAGCTCGCGGCGGCCACGACGTGCTGCGTCGGATTGCCGGCGGCGAGATCAATTCCA
GGCAGCTCCCGGACAATGCGGCTCTGCTGGCCCCGAACGAAGGACTCGAGGTCAACCCCGGTGCCCGGGGTGCTGGTGC
ACCTGCCGATCGCACAGGTTGGCCCCAACCGGCCGCTTGATGCCCGGTGCGCAAGCCCGGCAGTTGCCAAACCCATC
GTGATCAGGCTCGGCTCGCGAGTTCGGCGAAGAAATGTTTCGCTGATCACCTACCATCGGCCA (SEQ ID NO. 78)

Clone Rv140

.....Rv140SP6.seq:.....
TCAACACGCCGCCAGCCACCACGCGCGGTGCGGCGCGGGCCCGGCTCCAGGCTNCTCCGCTCGGTGATGGCAGG
CCACCGCGACACCACCGGCTGCGCTACGTGAGCCATACCGGGCGGAGCTACATCGGCCCGGCCAGTGTTCGG
GCCCTCTCGCCAGGTGAGGTGACACCGATTTGCGCATCCGACGCCGACCCCTGCGACGACAGAACCAGCGGCCCTA
CCCACTGCTTGTGCGGCGGGGGCCAAAGAACCAGCTTGNCATCCTGCCACAATTGGCCGGCGCCCG (SEQ ID NO. 79)

.....Rv140T7.seq:.....
CAGGCATGCAAGCTTCACGTCCGTACGGCTCGGGTACGCTTCGGTCGAGTGTCGAGTGATAGATGACGACCGGGAC
CTCGTCGGCATCTTCCATAGCCCGCCACACCTTCAGTTGCTACCGGAATCCAACCGGTAGAAGGTGGCCAGCGCTC
GGCATTGGTCATCGGGATATGCCGCTCGGGACGGTCAGAGCCCTCGGGTCCGGCCAGCACTCCGAGGCTTCGTCGGG
GTGGTCGCGACGCGCATGGGCCACCATCGCATTACCAGGTCTGCGCAATCACCAGCACGTAGACGGTTCTTTCTTCT
AAGCAACAC (SEQ ID NO. 80)

Clone Rv141

.....Rv141SP6.seq:.....
AATATTCAAGCTTTTCGGCGGAAACGGACNCCTTGCGAACATTGATAACAAAATAGAAATCATTGATGGTTTGAGTCAC
CAGGCCGATCAAGCCTTCGCCGAGCCAAATTCGAATCAAGAGGCCCAAGCCCGTACCAATCAGCCCGGCAACGAGGGA
TTCCGTCNTTATCAGCCNAAATAACTGCTCTCGGGTACCACCCAAACAGCGCAATATGGCGAAAAACGGTCGCCGTTG
CACAACATTAAATGTCTCGGTATTGTTGATTAAAAAGATACCCACCACCAGGGCAATCCAATGAGAGCGGTTAAATT
GACCGTAAAAACCTCCCGTCATCTGTTT (SEQ ID NO. 81)

.....Rv141T7.seq:.....
CAGGCATGCAAGCTTGCTGCATCTTCTGTGACTGCTCCCGAAACCTGGGGGTGTGCTGCTGTGATGCACGGCATA
CGGACATCCTTCCCCTGATACCCGCGGTGCAACCAGCCAGTGTCCATCATCAGGGGTCAACCCCGGCCAAGGGCGAC
GGCAGGCCAAGTTCCGCCAGCCGTTAACCTAGTGCTGTTAGCTTCATTTGCTGCGAGCAAAACAGCTGGTCGGCCGTTA
GGAAGTGAATTGAACTCAACCGATTTGGTGCCGCCGTAAGTGTCTGTCTGCGGGTGCGCTGGTGTGTCCGCGTGT
GGTAACGACGACAATGTGACCGGGGAGGTGAACCACTGGCCAGGCGTCCGCGAAAGTCCATTGCNNGGGGAAGAAG
ACAC (SEQ ID NO. 82)

Clone Rv142

.....Rv142IS1081.seq:.....
GAAAGTGCCTCAAGGTGTTGGTGAACTCGCTGGACGGTCCCCAGGATGTTGGCAGCACATTACCCGGACATGACCGG
AGCAAGACCGGACATCTCCCATACCGTCGTGCGCGTGTACATCCGTAGCCCGTCCTGGCAGGTGCTGGGTGAACAA
AATCAGCCCAACACCTGCCACGACGAAGAAGCGGGTTGCGCTGGCATGTCTTGTGCGCTCGGCGATCGAATTCTACGA
ATTCTTTATCTACGGGACCGCTGCGGCGCTGGTGTTCACCGTGTCTTCCACACCTGGATCCACGGTGGCCGC
CGTGGCCTCCAAGGGGACATTTGCTGTGGCGTTCCTATCCCGGCCGTTGCGCGCGGCCGTCTTTGGATACTTTGGAGA
CCGCTCGGCCGCCAGAAGACCCTGGTCGCCACACTGTTGATCATGGGCCTGGCAACCGTGACTGTTGGGCTGGTTCC
ACGACAGTGGCCATCGCGC (SEQ ID NO. 83)

.....Rv142SP6.seq:.....
ATATTCAAGCTTTGTACACCAAGTGTTCGACCAANCGCTCCATCCGGCGAGTGGATACTCCAGCAGGTAGCAGGT
CGCCACCACGCTGGTCAGTGCCTTCATCTCGCTTGGCGCGCTGCAGCAGCCAGTCCGGGAAATAGCTGCCCTGGCG
CAGCTTGGGGATCGCGACGTCGATGGTTGCGGCACGGGTGTCGAAATCACGGTGGCGGTAGCCGTTGCGCTGATTGGA
CCGCTCATCGCTGCGTTGCGGTAGCCNCCCGCACAGGGCGTGGCTTCAGCCCCATCCAAGGCGGCGATGAACG
TCGAGAGCAGCCCGCGCAGCAAATCCGGGCTCGCTGTGCGAGTTGGTCAGCCAGAAGCTGCTCGGTGTCATAAGATG
AGAAGAGGTCACTGCGTCCTTCTTCG (SEQ ID NO. 84)

.....Rv142T7.seq:.....
CAGGCATGCAAGCTTTTTGAGCGTCTCGCGGGGCGAGCTTCGCCGGCAATTCTACTAGCGAGAAGTCTGGCCCCGATACG
GATCTGACCGAAGTCGCTGCGGTGCAGCCACCTCATTTGGCGATGGCGCCGACGATGGCGCTGGACCGATCTTGTG
CCGCTTGCCGACGGCGACGCGTAGGTGGTCAAGTCCGCTACGCTTGGGCTTTGCGGACGGTCCCGACGCTGGTC
GCGGTTGCGCCGCCAAAGCGCGGGTGGGTGCGGTGATGAATGCCCTACCGCCGCGCACTGCAGGCCAGTGCCCC
GGCGATGTCAGCCATCGGGACATCATGCTCGCTTCATACTCCTCGACCACTCCGCGGAACAGCTCCATTCGGGAC
GCCCAACGC (SEQ ID NO. 85)

Clone Rv143

.....Rv143SP6.seq:.....
ATACTCAAGCTTTTGGCTGGGTGCGCTTCCAATTGACGCTGCACCGCTATGGGTTGCAGCAGCGGCTGGCNCCGCACA
CCCCACTGGCCCCGGGTGTTTTCGCCCCGAACCCGGATCATGGTGAGCGAAAAGGAGATTNCCTGTTGATGCTGGGA
TTCGCCACCGCGAGGCCATCGACCGATTACTCGCCACCGGGGTGCGAGAGGTGCCGAGTCCCGCTCCGTCGACGTC
CCGACGATCCATCCGGCTTCGCGCTGCGGTGGCGGTAGCCGTCGATGAAATCGCTGCCGGCCGCTACCACAAGGTGA
TTCTGTCCCGTTGTGTCCAAGTGCTTTTCGCGATCGACTTCCGTTGACCTACCGGCTGGGGCGTCGGCACAACACC
CGGTGAGGTGCTTTTTGTTGAGTGGGCGGAATCCGTGCTCTGGGTTACAGCCCCGAACCTCGTCACGGCGGTGCGCC
GCCGAC (SEQ ID NO. 86)

.....Rv143T7.seq:.....
CAGGCATGCAAGCTTCAACCTATTGACGCTTGTGCGAACTGACGGCGCCCGCGCATGGCCAATCCGGAAGACCATCA
TTGGCAGTGGCCGGGCGTAACAGGTTCCAGCCCCCAGGTGCCGCTCGAACATGCGGTGCAACCCATTTCGAGG
CCGGCAGGGAAGACCGCGGAAGCCGCAAGGGCTGCAGTTCCGCGCCCAATAGTGTGTCGCGCAACCATGCGCT
CGAAAACCGCCGCGGCGAGTCAGCGCACCCGACGCGAGGTGAGAGACGTCGTGAGCGCGCCACATGGGTTGCCAAT
CGGCACGGCAGGTAGGCCGCGCAACCCCAACGCTGGTGCATGCCAGGTCCGCGAGGAGGCCACCAACC

(SEQ ID NO. 87)

Clone Rv144

.....Rv144SP6.seq:.....
ATACTCAAGCTTCCCGGCCGAGGTGACGGCGCGGCTAGCGCCACTTGATGCCGACCCGATCGACGGNCGTTGGTC
GGGTTGACTGGCCGCGCGGCGAGCAGGGCGTCAACCGCGGCCGACGTCGGCGGCCGTACCGGTGCGCCATTGCC
CGGGCGGGAGTCGTCGAGCTGACCACGTTAGACAAGTCGGCGCTGGCCGTGCAAGACAAACGTGTGGGTGTGAGGC
CGCGGAGAAGGCGNCGGCGACGTCCTCGGTTTCGTCGTAGAGATACGGGAACGTCCAGCCGTGGCGCGCGGCTCGGC
GACCATCTGATCGGGCCGTCCTGCGGTAGGTGACCACTCTTACTGGAGATACCGACCATCGGGACCCCTTTGATC
GGCGAGGTCCCGGCCGACCGTGGCCAATCCGGCGGCGACGTCGCGCCGTACCGGCCAGTGTTT (SEQ ID NO. 88)

.....Rv144T7.seq:.....
CAGGCATGCAAGCTTTANCANATCAACCCCGCCCCGACACGACCGACAGATGTCGATGCCATCGAGGTGAATGT
CGAATGGCNCAACCATCTGGCGACCGCGACACCGGCAACATGGGTACCGGCGATTTCCGGTGCCAATGCCGACCC
GACGGGCGCTCTACCGCAGGTGACCTCGATCAGCGAGACCGCGGCCGTTATACTCAGCACCCCTACCGTGTCA
CGCCCAAAACGGCGCTGGTGGTGTGATTCGGGAGTGACCCCGCACCCAGTGTGTCGCGGATCCGCGGACCAATCC
CGCACCCAGTCGCCAAACCGAAATCACCGTGTGCGGTGGTAACTGACACCGACAGTAACGTCACTACGGCCGCC
ACGGCGACCGCAACCAACGACGACATGATGATCGGCTG (SEQ ID NO. 89)

Clone Rv145

:::Rv145SP6.seq:::

ATATTCAACCTTGCACACATTGACGATACCTTGGTCACGAGACCCCAAAAGCTGGCCTCCACCGCGCGCCGGGGACCA
CGGTACATACCTTGANNNGCTTTTCGATCGTTGATGCTGCGTCTTGGTCCGCGGAAACCGCAGGCTGGCATATGCACGT
GGGCGCACTGGCGATCTGCGATCCCCACCGATTGCGCCGAATACAGCTTTCAGCGGCTCCCCAAGTTGATCATCGACC
GGCTGCCGGATATCCGCACTTGGCGTGGCGGGTACC CGCGCCCGCTCGGACTGGACCGGCGTGGTTCGTGAGG
ACCACGAAC (SEQ ID NO. 90)

:::Rv145T7.seq:::

CAGGCATGCAAGCTTCATGCCGCGGCATGATAGCCACATGCACGCAATCGAACTCAGCGAAACCGGCGGGCCAGGCG
TCTTACGCCACCTCACCAGCGCGCAACCTCAACCGGCCACGGAGACCTCCTGATC (SEQ ID NO. 91)

Clone Rv146

:::Rv146SP6.seq:::

ATACTCAAGCTTGATTTTGATCATCATGATGATCATCACCCGAATTGTGGTAGCCGCACTGGTTATCGTGGGTACCGT
CGTGCTTTCCATGGGCGCCTCTTTCGGGCTTTCCGTATTGGTCTGGCAGGACATTCTGGGTATCGAGTTGTACTGGAT
GGTGTGGCGATGTGCGGTGATCCTGCTCNTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCCGGTTGAAAGA
GGAAATTGGGCGCGGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGAGTGGTGACGGCTGCCGGCAT
GGTGTTCGCGGTTACCATGTCGTTGTTGTGTTTCAGCGATTTGCGAATTATTGGTCAGATCGGTACCACCATCGGCCT
GGGCTTGCTGTTTCGACACCCTCGTCGTGCCTCGTTCATGAAACCGTCCATTGCTGCCCTGCTGGGACCTGGTTCTGGT
GGCCGCTACGGGTGCGCCGCGCCCGGCAGTCAATCTTCCGCCG (SEQ ID NO. 92)

:::Rv146T7.seq:::

CAGGCATGCAAGCTTGGCGTGCCGTTCCAACCCGAATTGGCTTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTC
AACGACGACGTCGTCCGCGGGACACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTA
CAACGCCGCGCGGAACGCTTCCGCCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGAC
GGCATCGCCACCGGAGCGACGGCCAAGGCGGCGTGCCAGGTGCGCCGGGCGCACGGTGCGGACAACGTGGTGCTGGCG
GTCCCCATCGGCCAGACGACATCGTGGCGAGA (SEQ ID NO. 93)

Clone Rv147

:::Rv147SP6.seq:::

ATACTCAAGCTTTTACGGTGATCGCGCATCACCTGGTTCATGAACTGGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCA
ACATGAGCCAGCCTCTCGTCGGCGGTGCGGTGACGGTCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCCTGAAAC
CAGCTTCCATATCCCGCGACGAACGACGCCAGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCGTT
CTCCACCGACCGGGCCCGGGTGTGGGGTGTTCGGCGACCGGCAGCCANGTGGTCCACACTGCCGAAG

(SEQ ID NO. 94)

:::Rv147T7.seq:::

TAGTCGCTGACCGGTGCAGGTTTCGACNATGTGGTGCCGGTTCGGCGGCTACGTGCCATCGAGACACTGGCGCAGGCT
ATCGCACCCGTTATCGGCTACGAGCAAATCGCGGTATGCGTCTTGAGCATGAGTCGGCGACCGTCTCATGGTCGAC
ACCCACGACGGAAGACGAGATCGCCGCTTANCNTGTGTGCCGCGGATTATCAGGACTGACCTCCTGGCTGACCGGC
ATGTTTGGTCGCGATGCCTGGCGCCCGGCGGCGTGGTCTGGTCTGGCTCGG (SEQ ID NO. 95)

Clone Rv148

:::Rv148SP6.seq:::

ATACTCAAGCTTTCGCGGATACCGGCATGTGCGGCACATCCAGAACTTCTGGGGGGATCCGCTGACAGCGGCGGGA
TCCCAAAGTGCGGATGATCGGGCCGCTACGTCTGGTGTACCTCGTTCGGTAACAACGAAACCGAAGCGTATGACTCG
GTCCACGCGGTGCGGCACATGGTGGACACACACCGCCACCGCAGGGGTGAAGGCCTATGTACCGGTCCGGCAGCA
CTCAATGCCGACGAGCCGAGGCGGAGACAAAAGTATCGTAAGGTACCGCGATCAGGACATGGTGATCGCAGCA
ATGTTGCTAGTGATCTATCGCCCCGTAATTACCGCGGTTCTCGTCTTGATCATGGTCGGCATCGACCTCGGCGCAATC
CGCGGATTNCTCGCCTTGTGCGCCGACCACAACATTTTCAGCCTTTCAACATTTGCGACAACCTGCTCGTTCTCATGG
CGATTGCNGCGAAC (SEQ ID NO. 96)

:::Rv148T7.seq:::

CAGGCATGCAAGCTTGGCGTGCCGTTCCAACCCGAATTGGCTTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTC
AACGACGACGTCGTCCGCTGGACACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTA
CAACGCCGCGCGGAACGCTTCCGCCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGAC
GGCATCGCCACCGGAGCGACGGCCAAGGCGGCGTGCCAGGTGCGCCGGGCGCACGGTGCGGACAAGGTGGTGCTGGCG
GTCCCGATCGGCCAGACGACATCGTGGCGAGATTCCCGGGTACGCCGATGAAGTGGTGTGTTTGGCGACCGGCG
TTGTT (SEQ ID NO. 97)

Clone Rv149

.....Rv149SP6.seq.....
ATACTCAAGCTTTGGCATTGTGCACATTTCCACCCGCTGCTCTATTAATGCTGAGCCGCTAATTGTGACCCAGTCGG
GAAACACGCGGAGCACAAATTCACCGCAGCGCGGGGGCGGTTCAACTCACCATGGATCGCTCTCGTCGTCTGGTGC
TGGACAATCGTCGCTGTAGCGCGTCGCGAACACCTCAGCTTCTGCTGCCGCGGCTTCTCCGGCGATGGTAACCCCA
GGTTTCGCCCACGGTCTTACGTAGCAGTGCGACGCGGTGTTTCATCTGCATCGACCTGTTGACTCATCTGTCAAGGAT
GAAGGCGTACTGGGCGACTGCGCCTTCTGCCGCGCCAGGTCGGCAATCACCAGGATCTCAGAAACGAGCTGCGACTC
ACTCTTCCAGGCCACCCTGGCCGAAAGCTCGACATGGTCAATCCGGCCG (SEQ ID NO. 98)

.....Rv149T7.seq.....
CAGGCATGCAAGCTTGCGGGCGGAGTGGTTTCGACGGCCGCTCGCTTCTCGGCATCGGTTTGGGCTGTACCAGCAG
TTGGTAGTTCTTCACGTACTGTTGTCGAGCGTCGAGCCGCGCGCTGTGAGGTCGCCGAGCGGTATCCCGCCAG
GCCGGTCAGGGTGCCCTTCCAGTCCACGCGCTGTGGTCGGCGAACCCTTATCTCAATCGAGACGATCGCCAGCTT
CATCGTGTGGCGATCTTGTCCGAGGCGACCTCGAACCGCGCTGCGAGTACAGCCACGCGATCGTGTGCCCTTCG
GTCGACCATCGTCGATACCGCAGGCACTTGCCCTC (SEQ ID NO. 99)

Clone Rv14

.....Rv14SP6.seq.....
ATACTCAAGCTTCCCGGCGGCCAGTACCGAAAGCGGAACAGCTCGCGGCAGCCACGACGTGCTGCGTCGGATTGCC
GGCGGCGAAATCAATTCCAGGCAGCTCCCGGACAAATGCGGCTCTGCTGGCCCGCAACGAAGGACTCGAGGTACCCCG
GTGCCGGGGTCTGTTGTCACCTGCCGATCGCACAGGTTGGCCACAACCGGCCGCTTGATGCCCGGTGCGCAAGCCC
GGCAGTTGCCAAACCCAGCGTGATCAGGCTCGGCTCGCGAGTTCGGCGAAGAAGTGGCTCGCCTGATCACCTACCATC
GGCCAGGATCTGCGTGTATCACAACGCTCGCCAGGAGGTTGTTGTTGCTATCGACGGCCTTTAGCCAGATGTTT
GGAATCGACTATCCGATAGTGTCCGCGCAATGGACTTGATCGCCG (SEQ ID NO. 100)

.....Rv14T7.seq.....
AGCTTCGGTGTAGCCGATCACCGGAAGCCGCATGATCAGCCACGTTTCGCGCCGCCCGGCATACGGCGGCGTACCGAT
CTCCGCGTCATACACCCGCGGTAATCGCCGACGGTGCCGGTTCGCGAGCCGAAGGTGACGACGCTGATTGAATCGAG
TTCCAGGTCCAGCGGGTGGCGCAGCAACGGCGCGAGCTCAACGACGTCAATCAGTTGTGCTTTCTACGGTCACCGA
CCCGGTGACCGTAGTCGCGCGGTGCGCTCGGCCGAGAAGTTGACCGGCCACCACCGCGACACCGCTTTGACGCGGAC
GCCACCCCGGATCGGTTGTGGCCAAGTAATTGGGTATTCCATTTGACGGGACGCCGACCCCGCAGCCCCAGTAC
CGCCACGACACGCGCGGTGACCCACCACTGTACGAACACCAAGGCGACGCCGA (SEQ ID NO. 101)

Clone Rv15

.....Rv150SP6.seq.....
ATACTCAAGCTTCCGTGGCTTCGCCC GCCCTGCCGGTGGACTTCATGACAACGCGGGGGCGATTACCCCGCTACCG
CCAGCAGCATGACGGCGGTACCTAACACCGCCCGGATGCCTCGACGTGCCTCGATGTGCTCAGGAATCGCCCCGGC
ACCGCGATCTCGAGGATCACCAGCGTTACCCCGGCGAGCGGACACCGACAATTCGATACCGGCCACGCCGATCCGG
CCCTGGGCCAGCTGATTGGAGCTGGCG (SEQ ID NO. 102)

.....Rv150T7.seq.....
CAGGCATGCAAGCTTCCACATGTACGGATCCACGAACATCCCGTTGAACTGACAGGTGCGGCGCGGCTCGATCAGGCC
GGCCACTTGTCTACGCGGTTACCGAAGATCTCTTCGGTGACCTGCCCGCGCGGCCAGCTCGGCCCCAGTGCCCGGC
GTTGGCGCGCGCGGACGATCTTGGCGTCCACGGTGGTCCGGGTCTTGCCCGCTAGCACGATCCGCGAGTCGGCCGG
TCACCCGGGT (SEQ ID NO. 103)

Clone Rv151

.....Rv151SP6.seq.....
ATACTCAAGCTTCCAAGTCCCAAGTGTGATCATGGCCAAAGAGCTCGACAAAGCCGTAGAGGCGTTTCGGACCCGC
CCGCTCGATGCCGCGCCGTATACCTTCTCGCCGCCGACGCCCTGGTGCTCAAGGTGCGCGAGGCGAGCCGCGTCGTC
GGGTTGCACACCTTGATCGCCACGCGCTCAACGCCGAGGGTACCGAAAGATCCTGGGCATCCAGGTCACCTCCGCC
GAAGACGGGGCGGCTGGCTGGCGTTCTTCCGCGACCTGGTCGCCCGCGGCTGTCCGGGTGCGCTGGTCAACAGC
GACGCCACGCCGCGCTGGTGGCCGCGATCGGGGCCACCCTGCCCGCAGCGGCTGGCAGCGCT (SEQ ID NO. 104)

.....Rv151T7.seq.....
CAGGCATGCAAGCTTCAACGTAGGCGCGCTCGATAAATGACTCCGCCGCGCTTCGCACATCCTCGTAGCGATCCTTG
CGAGCAGGTCAACCGGGCGTCCCGTCGAGGACCGGTTTTTGGCGTGCAGCCACTGGCCGACACCTCGGGGGGTA
AGCGAATCCGAGAGCAGGAGGACGAGGTACGGAAGCTCGCCGAGCCGGTCTACCGCTCAGGGCGGATGTGCGCGGT
CGCCACCCGCGTACCGCCGATCGGACACCTGTATGACCGCGCGACGTC (SEQ ID NO. 105)

Clone Rv152

.....Rv152SP6.seq:.....
CGCGGCGGCGCATTACCCCGCTACCGTCAGCAGCTTGACGGCGGTAGCGAACACCGCCGGATGCAGCGCAGGTGCGT
CTATGTGCACACGGAATCGCCCCGGCACC GCGATCTCGAGGATCACCAGTGCCCCCCCCCTG (SEQ ID NO. 106)

.....Rv152T7.seq:.....

GGGATCGAGGAACAGCGCGTTGAACTGATAGGTGCGGCCCGGCTCGAGCAGGCCGGCCATTTGTTGATGCGGTTACC
GAAGATCTCTTGGGTGACCTGCCCCGCCCGCGGCCAGCTCGGCCAGTGCCCCGGCGTTGGCCGCCCGCGGCAGCATCTT
GGCGTCCACGGTGTTGCGGGGTGATGCCCCGCGAGCAGGATCGGCGAGCGGCCGGTTCAGCCGGGTGAACTTCGTTCGAGAG
CTTGACCTGCGGTGCGGGAGGCGAACACGGTTCGGTGCGTATCTCGACCAGGCCCGGGCAACCTCGGGGGTGGCGCC
GACGGTGAACAGGTTGCGCTGGCCACCGCGGTAGCCGCCGGCACTATGCCGATGCCAGGCCGCGGATCACCAGGTGC
GGTCAGTCGGGTGAGGATGTGCCCCGGCCCCAGGTGGAAGATCCAGCGGGCGCGGCCGCGTGGACACNGGTGATCTC
GTCCACCATCGACTTTCTGATCA (SEQ ID NO. 107)

Clone Rv153

.....Rv153SP6.seq:.....

TAACTCAAGGCTTGCGTTGAGGCCCGAGGCCCATCGACGGTTTGGCGGCCCTTAAATGCACTGAGGTGCTCAATTGACC
CCACAGCGGAAATGCCGACTATTCGACAGGCCTCCTTCGCCTTGGCTGCCGGAGAGGGGCTCCGCGGGAACCGCATGCA
GGTATATGACCTCGGTTTCTCGGGTGCTACCGCGTGCCTTGTGAGGATGAACTCGGCGTTGGAATTGTCCAGCCGGC
CCAATTTCATCGAGCGCAGATTGCTACACATGCCCGCGCGGACATACGCTTCACCGTGGATCTGCTCCACACGGACCG
CCCTGTGCGGATCCTGCTCACGGGTAAAGGAACCTACNTGGCNCCTCGGTGCC (SEQ ID NO. 108)

.....Rv153T7.seq:.....

CCTTCTGCGCCACCCACACCGTCAACGCCCGCGAAGTCGACGTCGTCCAGGCCATCGGCGGCCCTCACGGATGGATTGCG
GCGCGGACGTGGTGATCGACGCCGTGCGGCCGACCGGAAACCTACCAGCAGGCCTTCTACGCCCGCGATCTCGCCGGAA
CCGTTGTGCTGGTGCGGTGTCGCGACGCCGACATGCGCCTGGACATGCCGCTGGTTCGACTTCTTCTCTCACGGCGGTG
CGCTGAAGTCGTGCTGGTACGGCGATTGCTTCCGAAAGCGACTTCCCCACGCTGATCGACCTTGACCTGCATGGCC
GGCTGCCGCTGCAGCGGTTGTTTCCGAACGCATCGGGCTCGAAGACGTGAGGAGGCGTTCCACAAGATGCATGGCG
GCAAGGTATTGCGTTCGGTGGTGATGTTGTGATGGCCGCCATCGAGCGCGTCATACCCACGG (SEQ ID NO. 109)

Clone Rv154

.....Rv154SP6.seq:.....

ATACTCAAGCTTGATTTGATCATCATGATGATCATACCCGAAGTGTTAGCCGCGAGTGTTATCGTGGGTACCGT
CGTGCTTTCCATGGGCGCTCTTTTCGGGCTTTCCGTATTGGTCTGGCAGGACATTCTGGGTATCGAGTTGTAAGT
GGTGTGGCGATGTCGGTGATCCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCCGGTTGAAAAA
AGAAATTGGGGCCGGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGGAGTGTTACCGCTGCCGGCAT
GGTGTTCGCCGTTACCA (SEQ ID NO. 110)

.....Rv154T7.seq:.....

ATTGNCTTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTCAACGACGACGTCGTCCGCGGGACACACCTCGATGC
TGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGCTTCCGCCCGGGCGTGA
CCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATCGCCACCGAGCGACGGCCAAGGCGGCGTG
CCAGGTGCGCCCGGGCGCACGGTGCGGACAAGGTGGTGCTGGCGGTCCCAGTCGGCCAGACGACATCGTGGCGAGATT
CGCCGGGTACGCCGATGAGGTGGTGTGTTTGGCGACGCCGCGGCTTGTCTTCGCCGTGCGGCAGGGTTACCGCAACTT
CACCCAGACCTCCGACGAAGAAGTGGTGGCGTTTTCTGGATCGTGCTC (SEQ ID NO. 111)

Clone Rv155

.....Rv155SP6.seq:.....

ATACTCAAGCTTTTCCCGTCCGTATCGCCCCAAGCGCGTGAGGCCGAAGCGGCTGGTTACGACTCCCTGTTTGTGATG
GACCACTTCTACCAACTGCCCATGTTGGGGACGCCCGACCGCGATGCTGGAGGCCTACACGGCCCTTGGTGCGCTG
GCCACGGCGACCGAGCGGCTGCAACTGGGCGCGTTGGTGACCGGCAATACCTACCGCAGCCCGACCTGCTGGCAAAG
ATCATCACCACGCTCGACGTGGTTAGCGCCGGTCGAGCGATCCTCGGCATTGGAGCGGTTGGTTTGGAGCTGGAACAC
CGCCAGCTCGGCTTCGAGTTCGGCACTTTCAGTGACCGGTTCAACCGGCTCGAANAGGCGCTACAGATCCTCGAGCCA
ATGGTCAAGGTGAGCGCCAACGTTTTTCGGCGATTGGTACCCACCGA (SEQ ID NO. 112)

.....Rv155T7.seq:.....

CGGCCACCGGGGCCACTCCGCACAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCGCCGACTTTC
CGCGGTACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAATACTTCATCC
TGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACTACATCATTC

GCACGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGTTCAAC
CAAACCTTGAAGGTGATTGTTAACCTGGGCTACGGCGACCCGGCCTATGGTTATTCGACCTCGCCGCCCAATGTTGCGA
CTCCGTTCCGGTTGTTCCAGAGGTACGCCCGGTGCTCATCGCCGACGCTCTCGTCGCCGGGACCAGCAGGGAATCGG
CGATTCGCCTACA (SEQ ID NO. 113)

Clone Rv156

:Rv156SP6.seq:::

ATACTCAAGCTTGGGGTGGCGCTGTGCGTGGTGTGCTTGGCGGCGTGGTATCAACACCGCCACGAAATGGGGCAC
AAGAAGGATTCGCTGGAGCGGTGGCTGTCCAAAATCACCTCGCCAGACCTGCTACGGGCACTTCTACATCGAGCAC
AACCGTGGCCATCACNTCCGGGTGTCCACACCGGAGGACCCGGCGTGGCGCGGTTCCGGGAAACGTTGTGGGAGTTC
CTGCCCCGCGAGTTATCGGCGGCTTGCCTCGGCCGTTTCAATTGGAGGCCCAACGGCTGCGTGGCTCGGCTCGGCTCAGC
CCCTGGAATCCCATGACGTATCTGCGCAACGACGTGCNCAACNCGTGGCTGATGTCNGTGGTGTGTTGGGGTGGG

(SEQ ID NO. 114)

:Rv156T7.seq:::

TCCGACCCGACCGCGGCGAACGCTCAAAGGCACCTACTGGCACCAAGGCCCCACACGTCACCTGTGACCTCCTGCG
CCGACCCCGCCGAGGTCTTGGCGTTACACCGAACGGGCGAGCCGGGAGTCTGGTACGCATCGAACAAGAGCAAG
GTGCATGGGCGGAGTTGTTCCGCCACTTCGTGATGACGGGGTGGATCCATTGAGGTCCGTGCGCGCTCGGTCGAG
TGGCGGTACACTCCAGGTACTCGACCTCACAGACGAGAGGACTCGATCCCATCTAGGTGTGGACGAAACAGATCTTC
TGTCCGACGACTACACCACCCAGGCCATCGCCGCGCCGCGATGCCAATTGACGCGCTACTGGCCCCGGCGG
CGGCGCTCCCGGTTGTCAAACACTTTGCCGTGTTGTTTACGCACTGCCAACATCGAGCCGA (SEQ ID NO. 115)

Clone Rv157

:Rv157SP6.seq:::

ATGAAATAAGAAGAGCACATCCCTCAGTCGGTTATCATCACTAGCGCTCGCCGACCCGTTAACCAGATCATAGCGAG
CGAACTGGCGAGGAAGCAAAGAATATCTGTTCTGTGATAGCTTTACGCTCAGCGCAAGAAGAAATATCCCCGCG
GGAACAACCTCCAGGTAGAGGTACACACGCGGATAGCCAATTGAGAGTAATAAACTGTGACACTCACACCCTCATCAAT
GATGACGAATACACCCCGATATCCGGTCACATGACGAAGGGAAAGAGAAGGATATCATCTGTGACAACTGCCCTCA
AATTTGGCTTCCTTAA (SEQ ID NO. 116)

Clone Rv159

:Rv159SP6.seq:::

ATACTCAAGCTTGTGAACTCCTTCTGAATACCGGCCGGCCATCCACAGATGCCCGGAAGAACTTCCAGGTACCCAT
GGCGGCTGGATCAGGGGGCGGCACAGTTGGTCTTGTCTGCTGAGTGGCGTCTTGTCCGGCTTGGACGGGGCTCC
GACGGTACCGGAGGGCAGCGACAAACACTTATGCACTTGGGCGACCCGCGAGACGGTCCGACACCCATCCCGACGG
CACAAGCTCAGCCGCGGCGCTTGTCTTCTGTCGGATCGACATTACCCACTTCTGACCGGGCTTGGGCGAAGGAA
GCAGAA (SEQ ID NO. 117)

:Rv159T7.seq:::

GGTATAGTCGCTGACCGGTGCAGGTTTCGACAATGTGGTGCCGTTTCGGCGGCTACGTGCCATCGAGACACTGGCGCA
GGCTATCGACCCGTTATCGGCTACGAGCAAATCGCGGTATGCGTTCTTGAGCATGAGTCGGCGACCGTCTGTCATGGT
CGACACCCACGACGGAAAGACGAGATCGCCGTCAAGCATGTGTCCGCGGATTATCAGGACTGACCTCCTGGCTGAC
CGGCATGTTTGGTCGCGATGCCTGGCGCCCGCGGCGTGGTCTGGTGGCTCGGATAGCGAGGTGAGCGAATTCTC
GTGGCAGCTCGAAAGGCTCCTGCCGTGCCGCTTTTGCAGAAACGATGGCGCAGGTTACGGTTCGCGGGGGTGGCGG
CCTGGCGGCGGCCA (SEQ ID NO. 118)

Clone Rv15

:Rv15SP6D2.seq:::

GAACTATATNATACTCAAGCTTCAAGTCAATGTGCGCAAGCCCTGACGCTGGCCGACCAGGCCACCGCCGCGGAN
CCCTNTCTAGA (SEQ ID NO. 119)

:Rv15T7.seq:::

CTGTAGCCACCTGTGCCATCCCCGTATGCCGCACTCTGGTCACTCTCGGATCCGCTGACACCCCGCTAAGGCTGCTC
CTCTCGGTGCATTACCTACCGACGGCGAACNCCCCAGCTTTACGACTATCCGGATGACGGCACCTGGTTGCCGGCT
AACTTCACCGTCAGCTTGGACGGCGGCGTACCGTCGATGGCGCCAGCGGGGCGATGGCCGGGCGCGGACCGATTC
GTCNTCANCTGTGCGTGAATTTGCCGACGTCATCGTGGTGGTGTGGGCAACGTCGCGATTGAGGGCTACTCCGGC
GTCCGGATGGGTGTCGTCAAGCGCCCGCACCGGCGAGGCCGA (SEQ ID NO. 120)